

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	DB	ID	Description
1	3374	100.0	2478	19	AAAT99117	Helicoverpa armigera
2	3353	99.4	2478	15	AA058553	Sequence of Heliot
3	294	8.7	6536	19	AAV04471	Nudariella beta-11
4	294	8.7	6536	19	AAV04471	Nudariella beta v1
5	139.5	4.1	3695	20	AAAX0209	Enterococcus faeca
6	139.5	4.1	3695	24	ABN8194	E faecalis EF108 g
7	139.5	4.1	3840	20	AAAX0208	Enterococcus faeca
8	139.5	4.1	3840	24	ABN8193	E faecalis EF108 g
9	139.5	4.1	19031	20	AAAX3104	Enterococcus faeca
10	130.5	3.9	8496	23	ABL30162	Drosophila melanog
11	129	3.8	11739	20	AAAX13087	Enterococcus faeca
12	127	3.8	6592	23	ABL19215	Drosophila melanog
13	126.5	3.7	8277	22	AAAG31116	Human diagnostic a
14	126	3.7	1548	24	ABO90255	M. capsulatus gene
15	125.5	3.7	2748	20	AAAX1820	Talaromyces emerso
16	124.5	3.7	7035	23	AAAS4978	Staphylococcus aur
17	124	3.7	29139	23	AAAS5959	Propionibacterium
18	124	3.7	4403765	22	AAAT99663	Mycobacterium tube
19	123.5	3.7	2935	23	AAAS8066	DNA encoding novel
20	123.5	3.7	265118	22	AAAH1257	Pyrococcus abyss
21	122	3.6	47981	22	AAFP0757	Micromonospora meg
22	121.5	3.6	21500	23	AAAS9633	Propionibacterium
23	121	3.6	1724	24	ABO68825	Listeria monocytog
24	121	3.6	2721	6	AAAN50114	DNA sequence encod
25	121	3.6	4403765	22	AAAT99663	Mycobacterium tube
26	121	3.6	4411529	22	AAAT99682	Mycobacterium tube
27	120.5	3.6	3410	22	AAAD17326	Streptococcus agal
28	120.5	3.6	4493	20	AAAX3610	Human ontherin enc
29	120.5	3.6	4493	20	AAAX3610	Cadherin-like poly
30	120.5	3.6	38734	20	AAAZ32020	Human MERT1 relate
31	120.5	3.6	38734	22	AAAG30077	AL021529 cdNA clon
32	120	3.6	2798	20	AAAX0207	Enterococcus faeca
33	120	3.6	2798	24	ABN8192	E faecalis EF107 g
34	120	3.6	3078	20	AAAX0206	Enterococcus faeca
35	120	3.6	3078	24	ABN8191	E faecalis EF107 g
36	119.5	3.5	4278	23	ABNL30183	Drosophila melanog
37	119	3.5	2907	22	AAKS52261	Human polynucleoti
38	119	3.5	5397	23	ABLT29757	Drosophila melanog
39	119	3.5	5982	24	ABO69372	Listeria innocua D
40	119	3.5	37856	21	AAAL11992	S. cellulosum DNA
41	119	3.5	1163020	24	ABO677197	Listeria innocua c
42	119	3.5	3011208	24	ABO69245	Listeria innocua D
43	118.5	3.5	2034	24	ABO70603	Listeria monocytog
44	118	3.5	1590	21	AAAT12883	Aspergillus oryzae
45	117.5	3.5	4776	20	AAAZ33707	S. erythraea pFL37

RESULT 1

AAAT99117 standard; cDNA: 2478 BP.

AAAT99117;

08-JUN-1998 (first entry)

Helicoverpa armigera RNA2 encoding coat proteins p71 and p17.

Vaccine; coat protein; p71; p17; insecticide; Ig-like domain; ds.

Helicoverpa armigera.

Location/Qualifiers

283..756

/\*tag= a

/product= p17 coat protein

ALIGNMENTS

FT CDS 366..2309  
 FT /tag= b  
 FT /product= p71 coat protein  
 XX MO9746666-A1.  
 XX 11-DEC-1997.  
 XX 02-JUN-1997; 97WO-AU00349.  
 XX 31-MAY-1996; 96AU-0000234.  
 XX (CSTR ) COMMONWEALTH SCI & IND RES ORG.  
 XX Gordon KH, Hanzlik TN;  
 XX WPI: 1998-042175/04.  
 XX P-PSDB: AAM34534, AAM34535.  
 XX Modified small RNA viruses and virus-like particles - have altered  
 XX or substituted Ig-like domains to modify host cell tropism, useful  
 XX as insecticides and in medicinal applications  
 XX Disclosure: Figure 1: 41pp: English.  
 XX  
 XX The sequence is that of a cDNA encoding RNA2 of the viral genome which  
 XX putatively codes for coat proteins p71 and p17. The p71 coat protein  
 XX includes an Ig-like domain which can be used in the production of  
 XX virus-like particles (VLP). The VLPS can be used in vaccines where the  
 XX Ig-like domain has been altered so that the VLP presents a surface  
 XX located antigen which is used to elicit an immune response in a host  
 XX organism. The gene can also be used controlling the proliferation of a pest  
 XX insect and potentially as medicinal delivery agents for cancer treatment  
 XX and gene therapy.  
 XX  
 SO Sequence 2478 BP: 516 A; 854 C; 607 G; 501 T; 0 other:  
 Alignment Scores:  
 Pred. No.: 3,27e-274 Length: 2478  
 Score: 3374.00 Matches: 647  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 19 Gaps: 0  
 US-09-677-653A-50 (1-647) x AAT99117 (1-2478)  
 Oy 1 MetGlyAspAlaGlyValAlaSerGlnArgProHisAsnArgGlyThrArgAsnVal 20  
 Db 366 ATGGAGATGCTGGAGTGGCTGCACAGCGACCTCACACCGTGGGAAACCGGTAACTT 425  
 Oy 21 ArgValSerAlaAsnThrValThrValAsnGlyArgAsnGlnArgArgThrGly 40  
 Db 426 CGGCTGACGGCCCAACACCTCACCTCAATGGTAGAAGAACCAAGGGGTGGACGGGA 485  
 Oy 41 ArgGlnValSerProProAspAsnPherThrAlaAlaGlnAspLeuAlaGlnSerLeu 60  
 Db 486 AGGCAAGTTTCTCCCTGACAAATTTCACCGCTGCTGCACAGACACTGCGGAAGCCCTT 545  
 Oy 61 AspAlaAsnThrValThrPheProAlaAsnIleSerSerMetProGluPheArgAsnTrp 80  
 Db 546 GACGCCAACACCGCTACCTTCCCGCTAACATCTACATGCCCCGAATTCCGGAATTGG 605  
 Oy 81 AlaLysGlyLysIleAspLeuAspSerAspSerIleGlyTrpTyrPheLysTyrLeuAsp 100  
 Db 606 GCCAAGGAAAGATGACCTCGACATCCGATTCATCGGTGCTACTTCAAGTAACTTGCAC 665  
 Oy 101 ProAlaGlyAlaThrGlySerAlaArgAlaValGlyGlySerLysIleProAspGly 120  
 Db 666 CCAAGGGGTGCTACAGAGTCTCGCGCGCGCTGCGGAGGACTCTCGAAGATCCCTGACGGC 725  
 Oy 121 LeuValLysPheSerValAspAlaGluLeuArgGluLeuTyrAsnGluGluCysProVal 140  
 Db 121 LLL

Db 726 CTCGTCAAGTTCCTCCGACGACGAGAAATAGAGATGCTAATACGAGAGTGCCTGTC 785  
 Oy 141 ValThrAspValSerValProLeuAspGlyArgGlnTrpSerLeuSerIlePheSerPhe 160  
 Db 786 GTCACTGACGTGTCCCTCCCTCCCTGACGGCCGCGCATGGAGCTTCGATTTCTCTTT 845  
 Oy 161 PrometPheArgThrAlaTyrValAlaValAlaAsnValGluAsnLysGluMetSerLeu 180  
 Db 846 CCGATGTTCAGAACCCGCTACGTCGCGCGTACGGAACGTGAGAACAGAGATGTGCTC 905  
 Oy 181 AspValValAsnAspLeuIleGluTrpLeuAsnAsnLeuAlaAspTrpArgTyrVal 200  
 Db 906 GACGTGTGACAGACCTCATCGATGCTCAACAAATCTCGCCGACTGGGTATATGCGTT 965  
 Oy 201 AspSerGluGlnTrpIleAsnPherThrAsnAspThrThrTyrTyrValArgIleArgVal 220  
 Db 966 GACTGTGAACAGTGAATTAATCTCACAAATGACACACCTACTACTCCGCAATCCGCTT 1025  
 Oy 221 LeuArgProThrTyrAspValProAspProThrGluGlyLeuValArgThrValSerAsp 240  
 Db 1026 CTACGTCCAACCTACAGAGCTTCCAGACCCACAGAGGGCTGTGTCGACAGTCTCAGAC 1085  
 Oy 241 TyrArgLeuThrTyrLysAlaIleThrCysGluAlaAsnMetProThrLeuValAspGln 260  
 Db 1086 TACCGCCCTCACTTATAGCGATTAACATGTGAAGCCCAACATCCACTCGTCACCAA 1145  
 Oy 261 GlyPheTrpIleGlyGlyGlnTyrAlaLeuThrProThrSerLeuProGlnTyrAspVal 280  
 Db 1146 GCGTTTGGATGGCGGCGGACAGTACGCTTCACCCGACACTACCGAATGACAGCTC 1205  
 Oy 281 SerGluAlaTyrAlaLeuHisThrLeuThrPheAlaArgProSerSerAlaAlaLeuLeu 300  
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 Oy 301 AlaPheValTrpAlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyThrProAlaTrp 320  
 Db 1266 GCGTTTGTGTGGGACGTTTGGCACAGGTGGCACCTGCGCTGCAGGCACTCCACCTGG 1325  
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 Oy 341 GlySerValSerTyrValLeuProGluGlyPheAlaLeuGluAlaTyrArgProAsnAsp 360  
 Db 1386 GCGTCGCTAGCTAGCTTCCCTGAGGGGTTCGCCCTTGACGCGCTACACCCGAAGCAGC 1445  
 Oy 361 GlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgIleValAlaVal 380  
 Db 1446 GGCTCTTGGACCGACTTCCCTTCCGAGAGACACCGCTCACTTCCGGCAGGTCCGCGTC 1505  
 Oy 381 AspGluValValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPheThrVal 400  
 Db 1506 GACGAGGTGCTGTGACCAACACCCCGCGCGGCGGAGGCGCCCACTTCAACCGTG 1565  
 Oy 401 ArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuLeuGlnThr 420  
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 Oy 421 ArgProSerSerArgArgLeuGluLeuProMetProProAlaAspPheGlyGlnThrVal 440  
 Db 1626 CGACCCTCTCTGTAAGGTCCGAACCTCCCTATGCCACCGTGCATTTGGACAGCGGTC 1685  
 Oy 441 AlaAsnAsnProLysIleGluGlnSerLeuLeuLysGluThrLeuGlyCysTyrLeuVal 460  
 Db 1686 GCCAACAAACCCGAAAGATGACAGATGCTCTTAAAGAAACCTTGGCTGATTTGGTGC 1745  
 Oy 461 HisSerLysMetArgAsnProValPheGlnLeuThrProAlaSerSerPheGlyAlaVal 480  
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 Oy 481 SerPheAsnAsnProGlyTyrGlyGluArgThrArgAspLeuProAspTyrThrGlyIleArg 500  
 Db 1806 TCCTTCAACAAATCCGGGTTATAGCGCACACGCGACTCCGGAATACACTGTGATCCGT 1865

QY 501 AspSerPheaspGlnasnMetSerThrAlaValAlaHisPheargSerLeuSerHisSer 520  
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 QY 521 CysSerIleValThrIysThrTYrGlnGlyTYrPgluGlyValThrAsnValAsnThrPro 540  
 DB 1926 TGCAGTATGCTCCTACTAAGACTTACAGAGGTGGAGAGCGCTCAGAACGTCACACGCCCT 1985  
 QY 541 PheGlyGlnPheAlaHisAlaGlyLeuLeuLysAsnGluIleLeuGlyLeuAlaAsp 560  
 DB 1986 TTCGGCAATTCGCGACGCGGCGCTCTCAAGATGAGAGATCTCTGCTCGCCGAC 2045  
 QY 561 AspLeuAlaThrargLeuThrIysValTYrProAlaThrAspAsnPheAlaAlaVal 580  
 DB 2046 GACCTGGCCACCGCTTCACAGGTGTCTACCCGCGCACTTCCGCGCGCTT 2105  
 QY 581 SerAlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGluAlaThrSerSerIle 600  
 DB 2106 TCGGCTTCGCGCGAAGCATGCTCTCGCTGTAAGTCGAGGCGAAGCTCTCCATC 2165  
 QY 601 IleLysSerValGlyIuThrAlaValAlaGlyAlaAlaGlnSerGlyLeuAlaLysLeuPro 620  
 DB 2166 ATCAAGTCCGTTGGCGAGACTGCGCGCGCTCAGTCCGCGCTCGGAAAGCTACCC 2225  
 QY 621 GlyLeuLeuMetSerValProGlyLysIleAlaAlaAlaArgValAlaArgAlaArg 640  
 DB 2226 GGACTGCTTAATGATGATACAGGAGAAATTCGCGGCTGCGCGCGCGCGCGCG 2285  
 QY 641 ArgArgAlaAlaAlaArgAlaAsn 647  
 DB 2286 CGCGCGCGCGCTGCTGCTGCAAT 2306

RESULT 2  
 AA058523  
 ID AA058523 standard; DNA; 2478 BP.

AC AA058523;  
 DT 12-SEP-1994 (first entry)  
 DE Sequence of Heliothis armigera RNA 2 which encodes P17 and the  
 DE capsid proteins precursor P71.  
 XX KW HasV, RNA 1; small RNA virus; P17; P71; SS.  
 OS Heliothis armigera stunt virus.  
 XX FH Key Location/Qualifiers  
 FT CDS 283..753  
 FT /tag= a  
 FT /product= p17  
 FT 366..2309  
 FT /tag= b  
 FT /product= P71  
 XX PN MO9404660-A.  
 PD 03-MAR-1994.  
 XX PF 13-AUG-1993; 93WO-AU00411.  
 XX PR 14-AUG-1992; 92AU-0004081.  
 PR 08-JUL-1993; 93US-0089372.  
 XX PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 PA (PACI-) PACIFIC SEEDS PTY LTD.  
 XX PI Christian PD, Gordon KHJ, Hanzlik TN.  
 DR WPI; 1994-083180/10.  
 DR P-PDB; AAR49661, AAR49662.  
 XX

PT Small RNA virus capable of infecting insect species, e.g.  
 PT Heliothis - and transgenic plants contg. viral nucleic acid, for  
 PT protection against insect pests

XX Disclosure; Figure 2; 183pp; English.

CC The inventors claim a virus comprising a genome hybridisable with  
 CC the nucleotide sequence of RNA 1 or RNA 2; pref. the sequences are  
 CC those given in Figs 1 and 2 of the specification. As isolated  
 CC protein or polypeptide prepn. of the proteins or polypeptides  
 CC derivable from the virus are also claimed.

CC H. armigera larvae were raised and viral RNA was extracted. The virus  
 CC RNAs were reverse transcribed into cDNA. Clone hr236 contains about  
 CC 88% or RNA 2. RNA 2 encodes a protein of mol.wt.71,000(P71) which  
 CC contains the peptide sequences corresp. to those determined from  
 CC the two virus capsid proteins. This protein is therefore the  
 CC precursor of these capsid proteins. In addition, another major  
 CC translaton product of apparent mol. wt. 24,000 is obtd. This  
 CC protein is derived from a mol. wt. 17,000 reading frame overlapping  
 CC the slab of the capsid protein gene. The Mr 24,000 protein (referred  
 CC to as P17) may have a function in modifying or manipulating the growth  
 CC characteristics or cell cycle of HasV-infected cells.

SO Sequence 2478 BP; 516 A; 853 C; 608 G; 501 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	Matches:
1.92e-272	2478	644
Score:	3353.00	Conservative: 0
Percent Similarity:	99.54%	Mismatches: 3
Best Local Similarity:	99.54%	Indels: 0
Query Match:	99.38%	Gaps: 0
DB:	15	

US-09-677-653A-50 (1-647) x AA058523 (1-2478)

QY 1 MetGlyAspAlaGlyValAlaSerGlnArgProHisAsnArgArgGlyThrArgAsnVal 20  
 DB 366 ATGGGAGATGCTGGAGTGGCGCTCAGACGACCTCACAACCGTCGCGAACCCTGAACGTT 425  
 QY 21 ArgValSerAlaAsnThrValThrValAsnGlyArgArgAsnGlnArgArgArgGly 40  
 DB 426 CGGGTCAGCGCCCAACACCGTCACCGTCAATGTGTGAAGAAACCAACGCGCTCGACCGGA 485  
 QY 41 ArgGlnValSerProProAspAsnPheThrAlaAlaGlnAspLeuAlaGlnSerLeu 60  
 DB 486 AGGCAAGTTCTCCCTCGCAATTCACCGCTGCTCACAAGACCTCGCGCAAGGCTT 545  
 QY 61 AspAlaAsnThrValThrPheProAlaAsnIleSerSerMetProGluPheArgAsnTrp 80  
 DB 546 GAGCCCAACACCGTCACTTCCCGCTACATCTCTGCAATGCCGGAATTCGGGAATTGG 605  
 QY 81 AlAlaGlyLysIleAspLeuAspSerAspSerIleGlyTrpIlePheLysLeuAsp 100  
 DB 606 GCCAAGGGAAGATCGACCTCGACTCGATTCATCGGTGATCTTCAAGTACCTTGAC 665  
 QY 101 ProAlaGlyAlaThrGlnSerAlaArgAlaValGlyIuThrSerLysIleProAspGly 120  
 DB 666 CCAGCGGGTCTACAGAGTGTGCGCGCGCGCGAGTCTGGAAGATCCCTGACGCGC 725  
 QY 121 LeuValLysPheSerValAspAlaGluIleArgGluIleIleTrpAsnGluGlyProVal 140  
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 QY 141 ValThrAspValSerValProLeuAspGlyArgGlnTrpSerLeuSerIlePheSerPhe 160  
 DB 786 GTCAGTACGTCGTCGCCCTCGAGCGCGCGCAGAGGAGACCTTCGATTTCTCTCTT 845  
 QY 161 PrometPheargThrAlaTYrValAlaValAlaAsnValGluLysnLysGluMetSerLeu 180  
 DB 846 CGAGTTTCAGAACCGCTACGTCGCGGTAGCAACCTCGAAGAACGAGAGTGCCTC 905  
 QY 181 AspValValAsnAspLeuIleGluTrpLeuAsnLeuAlaSprPAgTYrValVal 200

Db 906 GACGTTGTCACGACCTCATCGAGTGGCTCAACAATCTCGCGCATGCGCTTATGTCGTT 965  
 Qy 201 AspSerGluGlnTrpIleAsnPheThrAsnAspThrThrTyrtYrValArgIleArgVal 220  
 Db 966 GACTCTGAACAGATGATTAACCTTACCATTAAGACACAGGATGACTGCGCATCGCGCTT 1025  
 Qy 221 LeuArgProThrTyrtYrAspValProAspProThrGluGlyLeuValArgThrValSerAsp 240  
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 Qy 241 TyrArgLeuThrTyrtYrValAlaIleThrCysGluAlaAsnMetProThrLeuValAspGln 260  
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 Db 1206 AACGAGGCTACGCTTCGACACTTGCACCTTGCAGACATCCAGCGCGCTGCACCTC 1265  
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 Db 1326 GAGCAGGCACTCCTCGGGTGGTACCTCAGCTGGCGGCACACAGGTACTTCCAGCT 1385  
 Qy 341 GlySerValSerTyrtYrValLeuProGluGlyPheAlaLeuGluArgTyrtYrAspProAsnAsp 360  
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 Qy 381 AspGluValValIleThrAsnAsnProAlaGlyGlyGlySerAlaProThrPheThrVal 400  
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 Qy 421 ArgProSerSerArgArgLeuGluLeuProMetProProAlaAspPheGlyGlnThrVal 440  
 Db 1626 CGACCTCTCTCTGTAGGCTCGAAGCTCCCTATGCACTGCTGACTTGTGACAGAGGCTC 1685  
 Qy 441 AlaAsnAsnProGlyIleGluGlnSerLeuLeuGlyGlyThrLeuGlyCystTyrtYrLeuVal 460  
 Db 1686 GCCAACCAACCCGAGATCGACAGTGCCTTTTAAAGAAACCTTGGCTGCTATTGGTTC 1745  
 Qy 461 HisSerLysMetArgAsnProValPheGlnLeuThrProAlaSerSerPheGlyAlaVal 480  
 Db 1746 CACTCCAAATATCGAAACCCGCTTTCAGCTCAGCGCCAGCGACTCTTGGCGCGCTT 1805  
 Qy 481 SerPheAsnAsnProGlyTyrtYrGluArgThrArgAspLeuProAspTyrtYrThrGlyIleArg 500  
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 Qy 501 AspSerPheAspGlnAsnMetSerThrAlaValAlaHisPheArgSerLeuSerHisSer 520  
 Db 1866 GACTCATTCGACCAACAATGTCACACCGCTGTGGCCCACTTCGCTCACTTCCCACTTC 1925  
 Qy 521 CysSerIleValThrLysThrTyrtYrGlnGlyTyrtYrGluGlyValThrAsnValAsnThrPro 540  
 Db 1926 TGCAGTATCGTCACTAAGACCTACAGAGGTTGGAAAGGCGTCAACGACGCTT 1985  
 Qy 541 PheGlyGlnPheAlaHisAlaGlyLeuLeuLysAsnGluGluIleLeuCysIleuAlaAsp 560  
 Db 1986 TTCGGCAATTTCGCGACGCGGCGCTCCCTCAAGAAATGAGAGATCTCTGCTCGCGCAGC 2045

Qy 561 AspLeuAlaThrArgLeuThrGlyValTyrtYrProAlaThrAspAsnPheAlaAlaVal 580  
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 Qy 581 SerAlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGluAlaThrSerSerIle 600  
 Db 2106 TCTGCGCTTGGCGCGCAATGCTGTCTCCGCTCAAGTCCGAGGCAACGTCCTCATTC 2165  
 Qy 601 IleLysSerValGlyGlnThrAlaValGlyAlaAlaGlnSerGlyLeuAlaLysLeuPro 620  
 Db 2166 ATCAAGTCCGTTGGCGAGACTGCGCTCGCGCGGCTCACTCCGCTCCGGAAGCTACCC 2225  
 Qy 621 GlyLeuLeuMetSerValProGlyLysIleAlaAlaArgValAlaArgAlaArgAlaArg 640  
 Db 2226 GACCTGCTAATAGTGTACAGAGGAAGATTGCCCGCGTGTCCGCGCGGCGAGCGCGC 2285  
 Qy 641 ArgArgAlaAlaAlaArgAlaAsn 647  
 Db 2286 CGCGCGCGCGCTCGTGCAT 2306  
 RESULT 3  
 ID AAV04471 standard; cDNA; 6536 BP.  
 AC AAV04471;  
 XX 22-JUN-1998 (first entry)  
 DT  
 DE Nudaurelia beta-like virus RNA genome cDNA.  
 KW NBV; RNA virus; transgenic plant; insect resistance;  
 KW disease resistance; Nudaurelia cytherea capensis;  
 KW pine tree emperor moth; virus-like particle; vector; replicase;  
 KW capsid protein; ds.  
 OS Nudaurelia beta-like virus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 31..3732  
 FT /tag= a  
 FT /product= replicase  
 FT CDS 3884..5788  
 FT /tag= b  
 FT /product= capsid protein precursor  
 FT CDS 4219..5112  
 FT /tag= c  
 FT /note= "encodes protein of unknown function"  
 PN AU9724669-A.  
 XX  
 PD 04-DEC-1997.  
 XX  
 PF 02-JUN-1997; 97AU-0024669.  
 XX  
 PR 31-MAY-1996; 96AU-0000233.  
 XX  
 PA (CSTR ) COMMONWEALTH SCI & IND RES ORG.  
 PA (UIRH-) UNIV RHODES.  
 XX  
 PI Gordon KH, Hanzlik TN, Hendry DA;  
 XX  
 DR WPI: 1998-052736/06.  
 DR P-PSDB: AAM41935 AND AAM26785.  
 XX  
 PT Nudaurelia beta virus nucleic acid - useful for producing  
 PT recombinant virus, insect-resistant transgenic plants, etc  
 XX  
 PS Claim 3; Fig 1; 33pp: English.  
 CC This cDNA corresponds to the RNA genome of Nudaurelia beta-like  
 CC virus (NBV). cDNA fragments were generated by random-primed  
 CC reverse transcription of RNA of NBV collected from Nudaurelia



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DB 5467 TAGTGGACACCTCCGAAAGACAGCTGGCGTAAACAGTGGCGAACTTGGACCATCT 5526
OY 565 gieurthrglyValtyrProAlaThrAspAsnPhenAlaAlaValSerAlaPhenAla 585
DB 5527 GCACCCATTCCGATTCACCGAAGATACAGGATTCGGGGCCCTATTCGCGATGGTGC 5586
OY 585 aAsnMetLeuSerSerValLeuLysSerGluAlaThrSerSerIleIleLysSerValG 605
DB 5587 CAAGACCATAGCCCATGATTCCTGC-----TATGTGCGATCA----- 5623
OY 605 yGluThrAlaValGlyAlaAlaGlnSerGlyLeuAlaLysLeuProGlyLeuLeuMet 625
DB 5624 -----GCAGCCGGAGTGGCGAATGCGGTGACGCGACTCATAGAGAGCGACGAGAG 5676
OY 625 rValProGlyLysIleAlaAlaValAlaArgAlaArgAlaArgAlaArg----- 641
DB 5677 TGTAGCTCGTAATTCACCTCGAGAGGCGGCAAGAGAGCGACGTTGTCGCGAAT 5736
Y 642 ----ArgAlaAlaArg 645
DB 5737 CGCTGAGAGAGCCCGC 5752

RESULT 4
AAT99118
ID AAT99118 standard; cDNA; 6536 BP.
XX
AC AAT99118;
XX
DT 08-JUN-1998 (first entry)
XX
DE Nudarelia beta virus RNA genome encoding coat protein p70.
XX
KM Vaccine: coat protein; p70: insecticide; Ig-like domain; ds.
XX
OS Nudarelia beta virus.
XX
FH Key Location/Qualifiers
FT 31..3732
FT /*tag= a
FT /*product= undefined protein
FT 3884..5788
FT /*tag= b
FT /*product= p70 coat protein
XX
XX MO9746666-A1.
XX
XX 11-DEC-1997.
XX
XX 02-JUN-1997; 97WO-AU00349.
XX
XX 31-MAY-1996; 96AU-0000234.
XX
XX (CSTR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Gordon KH, Hanzlik TN;
XX
XX WPI; 1998-042175/04.
XX
XX P-PSDB; AAM34536, AAM34537.
XX
XX Modified small RNA viruses and virus-like particles - have altered
XX or substituted Ig-like domains to modify host cell tropism, useful
XX as insecticides and in medicinal applications
XX
XX PS Disclosure: Figure 2; 41pp; English.
XX
XX The sequence is that of a cDNA encoding the viral genome RNA which
XX putatively codes for coat protein p70. The p70 coat protein
XX includes an Ig-like domain which can be used in the production of
XX virus-like particles (VLPs). The VLPs can be used in vaccines where the
XX Ig-like domain has been altered so that the VLP presents a surface
XX located antigen which is used to elicit an immune response in a host
XX organism. They can also be used controlling the proliferation of a pest

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CC Insect and potentially as medicinal delivery agents for cancer treatment
CC and gene therapy.
XX
SQ Sequence 6536 BP; 1679 A; 1770 C; 1751 G; 1335 T; 1 other.

Alignment Scores:
Pred. No.: 2,82e-14
Score: 294.00
Percent Similarity: 37.50%
Best Local Similarity: 26.74%
Query Match: 8,71%
DB: 19 Gaps: 35

US-09-677-653a-50 (1-647) x AAT99118 (1-6536)
OY 2 GlyAspAlaGlyAlaAlaSerGlnArgProHisAsnArgArgGlyThrArgAsnValArg 21
DB 4014 GGGCAACACCGGGCGCGCAACAAACAACAGCTGCAGCAGAGAGCGGGGCTTAA 4073
OY 22 ValSerAlaAsnThrValThrValAsnGlyArgArgAsnGlnArgArgThrGlyArg 41
DB 4074 CTTCCCGCCGTAGTCGACCGATT----- 4097
OY 42 GlnValSerProProAspAsnPhenThrAlaAlaAlaGlnAspLeuAlaGlnSerLeuAsp 61
DB 4098 ----ACCAGCCCGCCAGATGGCGCAACCCCGAAC-----CAC 4130
OY 62 AlaAsnThrValThrPhenProAlaAsnIleSerSerMetProGluPhenArgAsnThrAla 81
DB 4131 GCGAACACCCGGGGTCAAC-CCGGCGTGC-----GACCGCGTGAAGGGGCT 4174
OY 82 LysGlyLysIleAspLeuAsp-----SerAspSerIleGlyTrpTrpLeuSerTyr 98
DB 4175 AAGGCAAGCGATGATGCAAGATCCATGGCAGCAGCATCAAGCATGATTCACGACTAT 4234
OY 99 LeuAspProAlaGlyAlaThrGlnSerAlaArgAlaValGlyGluTrpSerLysIlePro 118
DB 4235 CTAGACCCCGAGGAGATATCAAGACGACCTGCGACGAGCGG-----AAATTC 4285
OY 119 AspGlyLeuValLysPhenSerValAspAlaGlnIleArgGluIleTyrAsnGlnLys 138
DB 4286 GACGGCGCATCTCAGTCAACATATCGGTGTTGTTCAACACACGACGACGCGGCGCATAC 4345
OY 139 ProValValThrAspValSerValProLeuAspGlyArgGlnTrpSerLeuSerIlePhe 158
DB 4346 CCGGAGCTGAATTCACGACGCTACCGCTGATGGGGAGCTGGCCTCTACTACTATG 4405
OY 159 SerPheProMetPheArgThrAlaTyrValAlaValAlaAsnValGluAsnLysGlnMet 178
DB 4406 CATCTCCCGCTCTCAGGCGATCCGTTGTTTCATCACACGACGACGACGACGAA-- 4462
OY 179 SerLeuAspValValAsn---AspLeu-----IleGluTrpLeuAsnLeu 193
DB 4463 ---GTGAGATGACGACGACCGCATGCTGATGCGTTCGCGACAGATGG---AACACAG 4516
OY 194 AlaAspTrpArgTyrValValAspSerGlnGlnTrpIleAsnPhenThrAsnAspThrThr 213
DB 4517 ACGGACTGACCGAAGCGACG---TACCAACTTGGGGCGAAGTGGGGAAC-----GTG 4567
OY 214 TyrTrpValArgIleArgValLeuArgProThr-----TyrAspValProAspPro 230
DB 4568 TTTTACATGCTGCTC-----CCGACCGAAGCGCTGACGACGATACACCCCG 4615
OY 231 ThrGlu---GlyLeuValArgThrValSerAspTyrArgGluThrTyrLysAlaIleThr 249
DB 4616 ACTCAACTGGGTATCAAGGTTACTCGAGACTTACCGTCACTGACGCGGCTCA 4675
OY 250 CysGluAlaAsnMetProThrLeuValAspGlnGlyPheTrpIleGlyGlnTrpAla 269
DB 4676 GCGTACTTCACGACACCCATCTCTGATCAAGGAGTGGCGGTATGCGGAGTTC--- 4732
OY 270 LeuThrProThrSerLeuProGlnTyrAspValSerGluAlaTyrAlaLeuHisThrLeu 289

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Db 4733 ---CAACCGGCAAGAAACACAGAGAGAACCCGGACATAGTACCGGGACCAACCCAA 4789
QY 290 Thr-----PheAlaArgProSerSerAlaAlaAlaLeuAlaPhe 302
Db 4790 ACGGGGGGAACGTACAGCTCGGGGGGTCCAGGCGCAACATGACATGACATACG--- 4846
QY 303 ValTrpAlaGlyLeuProGlnGlyThrAla---ProAlaGlyThrProAlaTrpLeu 321
Db 4847 ATCGGGGACCAAGTCAGATTCGGGGGGCGACCAATCCCGCTACCCACGATGTCATGGGG 4906
QY 322 GlnAlaSerSerGlyGlyThrLeuThrTrpArgHisAsnGlyThrThrPheProAlaGly 341
Db 4907 CCGATGCCGGAGTCGGGAGCTGGTGTCCAGACTCGAAGCTGACATTCGACGTGGGA 4966
QY 342 -----SerValSerTrpValLeuProGlnGlyPheAlaLeuGlnArgTrpAspPro 358
Db 4967 AACACAATCACACATCACAGCCAGCCGTCACACAGGTCGGTG----- 5008
QY 359 AsnAspGlySerTrpThrAspPheAlaSerAlaGly---AspThrValThrPheArgGln 377
Db 5009 ---ACGGGAATGTGGCAATTCACAGCCAGCAGCGGAGCAGCAGCTGACC----- 5056
QY 378 ValAlaValAspGluValValValThrAsnAsnProAlaGlyGlySerAlaProThr 397
Db 5057 ---GTGGAC-----GCGGGAGCG----- 5071
QY 398 PheThrValArgValProProSerAsnAlaTrpThrAsnThrValPheArgAspThrLeu 417
Db 5072 ---ACTGTACGCGTTCCGAGAGAAATTGGACCCCTCGGAATGATCTGACGAGCATCAA 5128
QY 418 LeuGlnThrArgProSerSerArgArgLeuGlnLeuProMetLpProAlaAspPheGly 437
Db 5129 CTCATATCAAGTTCACCAAC-----GACATGAACCCCAATGATGACAGGC 5173
QY 438 GlnThrValAlaAsnAsnProLysIleGlnGlnSerLeuLeuLys-GlnThrLeuGlyCy 457
Db 5174 -----AACGCCAAGACCATTCAGTTCACACTAACGAAGCGGGCATTTAATAT 5221
QY 457 sTyLeuValHisSerLysMetArgAsnProValPheGlnLeuThrProAlaSerSerPhe 477
Db 5222 CCTG-----AGCGTCAATCCGTGTGAAATGACAAAT-GCGAGCTCTTA 5265
QY 477 eGlyAlaValSerPheAsnAsnProGlyTyGlnArgThrArgSp---LeuProAspT 496
Db 5266 TGGACCGGTGAT-----GAGACACCGAGGACAACTGTGTAGATT 5307
QY 496 yTrhGly-----IleArgAspSerPheAspGlnAsnMetSer----- 508
Db 5308 ACACGGGCAATTTGTGCACATCCAGGATACCATCGACAGCAACTTCCGATAGTTGCC 5367
QY 509 -----ThrAlaValAlaHis-PheArgSerLeuSerHisSerLysSerIleValThr 525
Db 5368 GTCGATGACCGTATGCTCTCATCATCAACCTGCTACTTGCAGAGCTTCGACGCTTCG 5427
QY 526 LysThrTrpGln-GlyTrpGlnGlyValThrAsnValAsnThrProPheGlyGlnPheAl 545
Db 5428 AAGCGATACCGCGGAGGGG-----CCTTGGGGGCCCTTCGCG 5466
QY 545 aHisAlaGlyLeuLeuLysAsnGlnGlnIleLeuLysLeuAlaAspSerLeuAlaThrAr 565
Db 5467 TAGTGGCAGACCTCCGAGAGGACGTCGGCTTAACAGTGTGCACTTGACACTTGACGATCT 5526
QY 565 gLeuThrGlyValTrpProAlaThrAspAsnPheAlaAlaValSerAlaPheAlaAl 585
Db 5527 GCACCCATTCGATACCCCGAGACGATACAGGATTCGGGGGCTTAATTCGCGATGGTGC 5586
QY 585 aAsnMetLeuSerSerValLeuLysSerGlnAlaThrSerSerIleIleLysSerValGl 605
Db 5587 CAACACATACCCAGATACCTGCG-----TATGTGCGATCA----- 5633
QY 605 yGluThrAlaValGlyAlaAlaGlnSerGlyLeuAlaLysLeuProGlyLeuLeuMetSe 625
Db 5624 -----GCAGCGGAGTGGCGAATGGCGTACGAGACTGCATTAAGACGCGGACGAGAG 5676

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QY 625 rValProGlyLysIleAlaAlaArgValAlaArgAlaArgArg----- 641
Db 5677 TGTAGCTCGAATTCACCTCGAGAGCGGCAACGAAGACGAGCTGTGGCGGAAT 5736
QY 642 ----ArgAlaAlaArg 645
Db 5737 CGCTCGAGAGGCCCGC 5752

RESULT 5
AAAX20209
ID AAAX20209 standard; DNA: 3695 BP.
XX
AC AAAX20209;
DT 20-APR-1999 (first entry)
XX
DE Enterococcus faecalis EF108 gene fragment.
XX
KW Enterococcus faecalis; infection; vaccine; immune response; diagnosis;
KM detection; attenuation; antigenic; ss.
XX
OS Enterococcus faecalis.
XX
PN MO9850554-A2.
XX
PD 12-NOV-1998.
XX
PF 04-MAY-1998; 98MO-US08959.
XX
PR 14-NOV-1997; 97US-0066009.
PR 06-MAY-1997; 97US-0044031.
PR 16-MAY-1997; 97US-0046655.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Bailey C, Choi GH, Hromocky J A, Kunsch CA;
XX
DR WPI; 1999-070095/06.
XX
DR P-PSDB; AAY00219.
XX
PT New isolated Enterococcus faecalis polynucleotides - used to develop
PT products for the detection of Enterococcus and for use in vaccines
PT for prevention or attenuation of Enterococcus infection
XX
PS Claim 1; Page 210-211; 301pp; English.
XX
CC The present sequence encodes an antigenic polypeptide fragment
CC isolated from Enterococcus faecalis. The present invention describes
CC genes, proteins and antigenic polypeptides isolated from E. faecalis.
CC The proteins can be used in vaccines for preventing or attenuating an
CC infection caused by a member of the Enterococcus genus in an animal.
CC They can also be used for detecting Enterococcus antibodies in a sample.
CC The nucleotide sequences can be used for detecting Enterococcus nucleic
CC acids. Products from the present invention can also be used for
CC screening compounds to identify agonists and antagonists of E. faecalis
CC protein activity.
XX
SQ Sequence 3695 BP; 1293 A; 790 C; 739 G; 873 T; 0 other;

Alignment Scores:
Pred. No.: 0.131 Length: 3695
Score: 139.50 Matches: 140
Percent Similarity: 31.38% Conservative: 95
Best Local Similarity: 18.69% Mismatches: 247
Query Match: 4.13% Indels: 267
DB: Gaps: 31

US-09-677-653a-50 (1-647) x AAAX20209 (1-3695)
QY 19 AsnValArgValSerAlaAsnThrValThrValAsnGlyArgArgAsnGlnArgArg 38
Db 1625 AACCGCAATGTCACCGAAGACTTGTGTACACCAACGCGCTAA----- 1669

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QY 39 ThrGlyArgGlnValSerProAspAsnPheThrAlaAlaGlnAspLeuIleArg 58  
Db 1670 -----ATCACACGGCCACAGGTTTCACCCAAAGTAAAGGATTTAC 1717  
QY 59 SerLeuAspAlaAsnThrVal-----ThrPheProAlaAsnIleSerSer 73  
Db 1718 AGC---GACGCCGTACACTTTCACAAACAGCAGCAGCTTACAGACCTTACACACAGGC 1774  
QY 74 -----MetProGluPheArgAsnThrAlaLysGlyIleAspLeuAspSerAsp 91  
Db 1775 GGTAAAGACCTACAGTTCAAGGTGGTACAAAGCCAGTCCATCTACACACATTGACA 1834  
QY 92 IleGlyTrpTyrPheLysTyrLeuAspProAlaGlyAlaThrCluSerAlaArgAlaVal 111  
Db 1835 ACT----- 1837  
QY 112 GlyIuTyrSerLysIleProAspGlyLeuValLysPheSerValAspAlaGluIleArg 131  
Db 1838 -----ACCAAGCGCCAGTTATCAAGTCCAGCTTACAGTACATGATGATTGAAAT 1888  
QY 132 GluIleTyrAsnGluGluCysProValValThrAspValSerValProLeuAsp 149  
Db 1889 GTGGGTATGAAGAAAGAACAGTTACAGACAGTGTATCCATCATGATGAACCTTGTG 1948  
QY 150 -----GlyArgGlnTrpSerLeu 155  
Db 1949 AATGAAAGGCGGCGCTTTCACACCGCGCTTAACCTTTAGTGGTAACTATGCGCAA 2008  
QY 156 SerIlePheSerPheProMetPheArgThrAlaTyrValAlaValAlaAsnValGluAsn 175  
Db 2009 ACTGACAGTGCCTAC-----TTAAGAACCGGATTTATATGAGCTGACCTCAAAAATAAT 2062  
QY 176 -----LysGluMetSerLeuAspValValAsnAspLeu 186  
Db 2063 GGTAAATGGCAATATACGTAAGTATTAATGATGATGATGATGATGATGATGATGAT 2122  
QY 187 IleGluTrpLeuAsn----- 191  
Db 2123 TTGAAAAAATATATATATGACACACCAATCAGTGTACACACAGATTACAGTTATATGTT 2182  
QY 191 ----- 191  
Db 2183 GATAAATATGACATCGACACCAACATAATATGTTGACAGATTCATATGACACAGCT 2242  
QY 192 -----AsnLeuAlaAspTrpArgTyrValVal----- 200  
Db 2243 CAAAGTACGAATCTGAATCTATAGATATGTGTACACAAACATAGCTCAGCTGTTTC 2302  
QY 201 -----AspSerGluIleTrpIleAsn 207  
Db 2303 GACCCAAATGTAGACACACAGAGTTGACCTTACGTAAGATCTCTTAACCTGCTAAT 2362  
QY 208 PheThrAsnAspThrThrTyr----- 215  
Db 2363 TTTGATTCAGATGCGACCTATTTTCTAATGCAAAATATAGACTTTTACACGCAATTA 2422  
QY 216 -----ValArgIleArgValLeuArgProThrTyrAspVal 227  
Db 2423 GATATAGTGGACACACAGAGTTAACTATCTTCTCGTATGTGTTTAAAGCCCAA 2482  
QY 228 ProAspProThrGluGlyLeuValArgThrValSerAspTyrArgLeuThrTyrIleVal 247  
Db 2483 CCTGGGATTAAGTCAAACTTGTG-----TACAAATCTACCTGCAACAA 2527  
QY 248 IleThrCysGluAlaAsnMetProThrLeuValAspGlyIlePheTrpIleGlyGln 267  
Db 2528 GTACACC-----GAAACCTTCGTGGAT-----GTCAACGGTGGCC 2560  
QY 266 TyrAlaLeuThrProThrSerLeuProGlnIleTyrAspValSerGluAlaTyrAlaLeuHis 287  
Db 2561 AAATCTACTGACCAACAGGCTTACCCAA-----GTTAACCAAGTACCAATGAAC 2611

QY 288 ThrLeuThrPheAlaArgProSerSerAlaAlaLeu----- 300  
Db 2612 ACTAACACCTTC---AAGTACACAGCGGCAAAAGCTTTACACGCGCATCTACAGGT 2668  
QY 301 -----AlaPheValTrpAlaGlyLeuProGlnGlyIleThrAlaProAlaGlyThrPro 318  
Db 2669 GGCAAAGCTATACGTTCACAAAGGTGGTATAAAGGAAACCAACCAAGTACGTTG--- 2725  
QY 319 AlaTrpGluGlnAlaSerSerGlyGlyTyrLeuThrTrpArgHisnclYThrPhe 338  
Db 2726 -----AACAAACAAACACT 2740  
QY 339 ProAlaGlySerValSerTyrValLeuProGluGlyPheAlaLeuGluArgTyrAspPro 358  
Db 2741 CCAAGCTTCATGCGAC-----TTGATGGC 2767  
QY 359 AsnAspGlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnVal 378  
Db 2768 AATGACGATATGACCCCATGTATAGGAAGAAATCCAAACAGCTGTCTCACATTAACT 2827  
QY 379 AlaValAspGluValValValThrAsnAsnProAlaGlyGlySerAlaProThrPhe 398  
Db 2828 CCACCAAAAGTGTATATACGAATACCAATGATATCTGACACACACAGTACGGAAT 2887  
QY 399 ThrValArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeu 418  
Db 2888 ACTAGCAAGACACC-----TTACAAATCTCACCTTG 2920  
QY 419 GluThrArgProSer---SerArgGluGluLeuPro-----MetProProAlaAsp 435  
Db 2921 AAAAAGGCGCCAAATGGTGCAGCTGTCTGACGATCCACCTTATGGAAGTGCACCA 2980  
QY 436 PheGlyIleThrValAlaAsnAsnProLysIleGluSerLeuLysGluThrLeu 455  
Db 2981 GAAGGAAACCAACAAATCAATCCCA---GTAAATAGTACCTTTGGACAGGGGGTT 3037  
QY 456 GlyCysTyrLeuValHisSerLysMetArgAsnProValPheGluLeuThrProAlaSer 475  
Db 3038 -----CCTTACCAAAATCGCTCTCATGCGC 3064  
QY 476 SerPheGlyAlaValSerPhe-----AsnAsnProGlyTyrGluArgThr 490  
Db 3065 AAAAAGTTTCAGTTGCTTTCACAACTCGCGCAACAGGAAACCAACACTGTTGAAA 3124  
QY 491 ArgAspLeuProAspTyrThrGlyIleArgAspSerPheAspGluAsnMetSerThrAla 510  
Db 3125 GCAGAGTGTATATGTTGTGTATTAAGATAGTACAGTGTGATATC----- 3175  
QY 511 ValAlaHisPheArgSerLeuSerHisSerCysSerIleValThrLysThrTyrGlnGly 530  
Db 3176 -----GTGAGATTTGCTCCAAATGATCAAGAGTGTGTACACCAACGACCCGAAGC 3226  
QY 531 TrpGluGlyValThrAsnValAsnThrProPheGlyGlnPheAlaHisAlaGlyLeuLeu 550  
Db 3227 TTCATCAGTGTGCAACCTTCAC-----TTGCGCAAGTGGCGGCTTCAGGAACTAAG 3280  
QY 551 LysAsnGluGluIleLeuCysLeuAlaAsp----- 560  
Db 3281 CAACAAACAGCTTGAAACAGCCGGGATTTACTACGTTAAAGGCAACAGGAATCCGTAT 3340  
QY 561 -----AspLeuAlaThrArgLeuThrGlyValTyr 570  
Db 3341 CTGGCGATTAAAGAAACGCAACCCAAATGTGAGCTTAAAGCGCACTGTCAACAA 3400  
QY 571 ProAlaThrAspAsnPhe-----AlaAlaAlaValSer 581  
Db 3401 TCAGCGCAGAGAGCTGTGCTACAGGACCCGTTATTTAGGGCGCGCGCTGTCTCT 3460  
QY 582 AlaPheAlaAlaAsnMetLeuSerValLeuLysSerGlu-----AlaThrSerSer 599  
Db 3461 AGCTTTACCAATTTACATATACCAACACGAGTTGAAATAATACGTCGTTCCAGAGTGC 3520  
QY 600 IleIleLysSerValGlyIuThrAla 608



Dn	3521	ATTTAGCTTAACAGCCAAACAACAGCA	3547
		: : :	
RESULT	6		
ID	ABN98194		
XX	ABN98194 standard; DNA: 3695 BP.		
XX			
PT	ABN98194;		
XX			
DT	05-AUG-2002 (first entry)		
XX			
DE	E faecalis EF108 gene fragment.		
KW	Enterococcus; vaccine; gastrointestinal disease; diagnosis; antibiotic;		
KM	gene; ds.		
OS	Enterococcus faecalis.		
PX	US2002045737-A1.		
NN			
PD	18-APR-2002.		
PF	04-MAY-1998; 98US-0071035.		
PR	04-MAY-1998; 98US-0071035.		
PA	(HUMA-) HUMAN GENOME SCI INC.		
PI	Choi GH, Bailey C, Bromocky A, Kunsch CA;		
PS	WPI: 2002-425450/45.		
DR	P-PADB; ABP43438.		
XX			
PT	New genes and polypeptides from Enterococcus faecalis, useful as		
PT	vaccines for preventing, treating or attenuating an infection caused by		
PT	a member of the Enterococcus genus in an animal, particularly E.		
PT	faecalis -		
XX			
PS	Claim 1; Page 194-196; 255pp; English.		
XX			
CC	The present invention provides the protein and coding sequences of a		
CC	number of polypeptides from Enterococcus faecalis. The proteins can be		
CC	used as vaccines for preventing or attenuating an infection caused by a		
CC	member of the Enterococcus genus in an animal, particularly E. faecalis		
CC	The polynucleotide is also useful for preventing or treating E. faecalis		
CC	Infection. The present sequence is a coding sequence of the invention.		
XX			
SO	Sequence 3695 BP; 1293 A; 790 C; 739 G; 873 T; 0 other;		
	Alignment Scores:		
	Prod. No.:           0.131         Length:         3695		
	Score:              139.50       Matches:        140		
	Percent Similarity: 31.38%       Conservative: 95		
	Best Local Similarity: 18.69%     Mismatches: 247		
	Query Match:          4.13%       Indels:         267		
	24             Gaps:           31		
Us-09-677-653A-50 (1-647) x ABN98194 (1-3695)			
OY	19 AsnValArgValSerAlaAsnThrValThlValAsnglyArgArgasnglnArgArgArg 38		
	:::::  ::                 :::		
Dn	1625 AACGGCAAAGTCACCAGAACCTTGTAACACACCAACGCCGTAA----- 1669		
OY	39 ThrGlyArgGlnValSerProCrocTropBapherThrlalaIalagInaspLeuAlagln 58		
	:::::::-:ARCACACCGCCCAACAGGTTCCACCCCAAGSTAAAAAACGGTAGATTACA 1717		
OY	59 SerLeuaspAlaasnThrVal-----ThrpeproAlaasnleaser--- 73		
	:::::		
Dn	1718 AGC--GACGGCTCACACTTCCAACAAGCAGCAGCCTTACACAGACTTACACAACAGGC 1774		
OY	74 -----MetProglunpheargAsnTrPalaysgLylysllleaspleuaspserAsps 91		
	:::    :::                  :::~::~		

Db	1775	GGTAAAGCACTCAAGTTCACAAAGTTGGTCAAAAGCAAGCAAGTCATCTCAACACATTGACA	1834
Qy	92	IIleGIuTrpTyRrPheuysTyRleuAspProAlaGIyAlaThGluserAlaArgAlaVal	111
Db	1835	ACT-----	1837
Qy	112	GIyGIuTrpSerIysIleProAspGIyLeuValIysPheSerValAspAlaGIuIleArg	131
Db	1838	-----ACCAAAAGGCCAAAGTTATCAAGTGAACCTACGATGACAAATGATGATTGGAT	1888
Qy	132	GIuIleTrpAsnGluGlyCysProValAlaThrAspValSerIleValProIleuAsp-----	149
Db	1889	GTGGTGTATGACAGACAGAACAGTTAGACAGAGTATCCATCGATCGATATGACACTTGTG	1948
Qy	150	-----GIyArgGIuTrpSerLeu	155
Db	1949	AATGAAAAAGGGGGGGCTTTCACACCGGGGTTACTTTAGTGAAGTACTATCGCGAA	2008
Qy	156	SerIlePheSerPheProMetPheArgThrAlaTyRValAlaValAlaAsnValGIuAsn	175
Db	2009	AGTACGAGTGCGTAC-----TTAAGAACCGATTATATGACGTCAACCTCAAAAATATAT	2062
Qy	176	-----LysGIuMetSerLeuAspValAlaAsnAspLeu	186
Db	2063	GGTAAATGGCAATATACGGTAACTATTAATATGATGATGATCCATGTCGCCAAGATTA	2122
Qy	187	IIleGIuTrpLeuAsn-----	191
Db	2123	TTGAAAAAATATATATATATGACACAAACATACAGTGCACAAACAGATTTACAGTTATGTT	2182
Qy	191	-----	191
Db	2183	GATAAATTAGCCATCGCACCAACAATAAATATGTGACAGCATTCAAATTAGACACAGCT	2242
Qy	192	-----AsnLeuAlaAspTrpArgTyRValVal	200
Db	2243	CAAAAGTACCATCTGAANAATCTATATAGATATGTGTACAGCAACAATAGCTCACTGGTTTC	2302
Qy	201	-----AspSerGIuGIuTrpIleAsn	207
Db	2303	GACCAATATGACACACAGAGGTTGACCTTACTGAGATCTCTTAACCTGCTTAT	2362
Qy	208	PheThrAsnAspThrTyRTyR-----	215
Db	2363	TTTGATTCAGATGGCAACCTATTTTCTTAATGCAATAATATAGACTTTTACACGCATTTA	2422
Qy	216	-----ValaGIuIleArgValLeuArgProThrTyRAspVal---	227
Db	2423	GGATATAGTGGCACACACAGAGATTAACCTATCTCTGATGTTCTTTTAAACCCAAA	2482
Qy	228	ProAspProThrGIuGIuLeuValArgThrValSerAspTyRArgLeuThrTyRysAla	247
Db	2483	CCTCGCATATAGTCAAAACTTGTC-----TAAAGTCACTCGCAAAACA	2527
Qy	248	IleThrCysGIuAlaAsnMetProThrLeuValAspGIuGIuIleThrPheTrpIleGIyGIu	267
Db	2528	GTCAAC-----GAAACTTCGTGGAT-----GTCAACGCTGCC	2560
Qy	268	TyrAlaIleuThrProThrSerLeuProGIuTrpAspValSerGIuAlaTyRAlaIleuHis	287
Db	2561	AAAAATCACTGCACCAACAGGCTTCACCCA-----GGTACCAAGTACCAATGMAAC	2611
Qy	288	ThrIleuThrPheAlaArgProSerSerAlaAlaIleu-----	300
Db	2612	AGTAAACACTTC---AAGTCAACAGCGGCAAAAAGCTTTACACGACAGTATACAGAGT	2668
Qy	301	-----AlaPheValTrpAlaGIuLeuProGIuGIyGIuThrAlaProAlaGIuTrpPro	318
Db	2669	GGCAAAATCTATACGTCTCCAAAGGCTGATTAAGGAAACCAACCAAGTACGTTG---	2725
Qy	319	AlaIleuGIuAlaIleSerIleGIyGIuTyRLeuThrTrpArgHisAsnGIuThrThrPhe	338
Db	2726	-----ACCAAAACAACAACACT	2740



QY 112 GtlyglutryserlylleproaspglyleuvallyspheSerValasplaglulearg 131  
 Db 1975 -----ACCAAGCGCAAGTTATCAAGTACCTAGACATGATGATTTGAAT 2025  
 QY 132 GtlyletrynsglucylcysprovalylthraspvalSerValproleuasp----- 149  
 Db 2026 GTGGTGTATGAAGAAACAGTTAGACAGTATCCATGATGCAATGAACTTTGG 2085  
 QY 150 -----GlyargclntrpSerleu 155  
 Db 2086 AATGAAAAAGGGGGCTTTCACACGGCGTTAACTTTAGTGGTAAGTACATGCGCAA 2145  
 QY 156 SerllePheSerPheProMetPheargthralaTyvalaValaalaasnValgluasn 175  
 Db 2146 AGTAGAGTGGTAC-----TTAAGACCGATTATATAGACGTGACCTCAAAAAATAT 2199  
 QY 176 -----LysglumetSerleuaspValValasnaspleu 186  
 Db 2200 GGTAAATGGCAATATACGGTAAGTATTAATGTAATGTAATGCCATTGCCCCAAGATTA 2259  
 QY 187 lIeGlutrpLeuasn----- 191  
 Db 2260 TTGAAAAAATATATATATGAGCAACCAATCAGTGTACCAACAGATTACAGTTAATGTT 2319  
 QY 191 ----- 191  
 Db 2320 GATAAATTCGCAATGCAACCACTAAATATGTTGACAGCATTCATTAATGACACAGCT 2379  
 QY 192 -----AsnleuAlaasptPrArgTyValaVal----- 200  
 Db 2380 CAAAGTAGCAATCTGAAATCCATATAGATATGTACAGACAAATAGCTCAGCTTTTC 2439  
 QY 201 -----AspSerGlucIntrpIleasn 207  
 Db 2440 GAACCAATATGACACACAGAGTGTGACTTATGTTCAAGAACTCTTAACCTTGCTTAAT 2499  
 QY 208 PheThrAsnAspThrThrTyTr----- 215  
 Db 2500 TTTGATTCAGATGGCACCTATTTTCTTAATGCAAAATATAGACTTTTTCACGCACTTA 2559  
 QY 216 -----ValArgIleArgValleuArgProThrTyArgspVal----- 227  
 Db 2560 GGATATATGGGACACAGGAGTTACTATCTTCGTAATGTTCTTTTAAAGCGCAA 2619  
 QY 228 ProAspProThrGlucIlyleuValaArgThrValSerAspTyArgleuThrTyRlysaIa 247  
 Db 2620 CCTGGCGATTAAGTCAAAACTTGTTC-----TACAAAGTCACTCGCAAAACAA 2664  
 QY 248 IleThrCysgluAlaasnMetProThrleuValasplnglyPheThrIleGllyglIn 267  
 Db 2665 GTACACC-----GAAAACCTCGTGAT-----GTCAACGCTGCC 2697  
 QY 268 TyraIaLeuThrProThrSerleuProGlnTyArgspValSerGluaIaTyraIaLeuHIS 287  
 Db 2698 AAAATCATCTGCACCAACAGCTTACACCAA-----GTTAACCAAGTACCAATGAAC 2748  
 QY 288 ThrleuThrPheAlaArgProSerSerAlaIaIaLeu----- 300  
 Db 2749 AGTAACACCTTC--AAGTACACAGGGCAAAAGCTTTACCGACGAGCATATACAGGT 2805  
 QY 301 -----AlaPheValTrpAlaIleuProGlnGlyTyThrAlaProAlaIleuThrPro 318  
 Db 2806 GGCAAGTGTATATCGTTCAAGGTTGTATMAAGGAAACCAAGCAAGTACGTTG--- 2862  
 QY 319 AlaTrpGlucIlaIaSerSerGlyTyRleuThrTrpArgHISasnGlyThrThrPhe 338  
 Db 2863 -----AACAAACACACACACT 2877  
 QY 339 ProAlaGlySerValSerTyRValleuProGlnGlyPheAlaIleuclnArgTyArgPro 358  
 Db 2878 CCAAGCTTCAATGCGAC-----TTTGATGGC 2904  
 QY 359 AsnAspGlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgInVal 378

Db 2905 AATGACGATATGACCCCATGTATAGAAAGAAATACCAACAGCTGTCTCACATTACT 2964  
 QY 379 AlaValaspluValValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPhe 398  
 Db 2965 CGACCAAAAGAGTATGATGAAATACCAATGTATCTGGACACACAGATCACGAAT 3024  
 QY 399 ThrValArgValProProSerAsnAlaTyThrAsnThrValPheArgsnThrleuLeu 418  
 Db 3025 ACTAGCAAGACACC-----TTACAAATCTCACACTTG 3057  
 QY 419 GluThrArgProSer--SerArgIleGluLeuPro-----MetProAlaIaSp 435  
 Db 3058 AAAAAAGGCCCAATGTGTCAGCTGTGTGACATCCCACTTATGGAAGTACACCA 3117  
 QY 436 PheGlyGlnThrValaIaAsnAsnProIlyleGluGlnSerleuLeuysgluThrleu 455  
 Db 3118 GAAGGAGAAACGCAAAATCAATCCCA--GTAATATGACACTTGTGACAGAGGGGTT 3174  
 QY 456 GlyCysTyRleuValHisSerIysMetArgAsnProValPheGlnleuThrProAlaSer 475  
 Db 3175 -----CPTTACAAATGCCGTTCTTATCGGC 3201  
 QY 476 SerPheGlyAlaValSerPhe-----AsnAsnProGlyTyRgluArgThr 490  
 Db 3202 AAAAAAGTTCACTTCCTTTCACACTCCGCGCAACGGAACCAACACTGTTTGA 3261  
 QY 491 ArgAspleuProAspTyThrIleArgAspSerPheAspIlaAsnMetSerThrAla 510  
 Db 3262 GCAGAGTGTGATATTTGGTGTATTAAGATAGTACAGTGATTAATCTTC----- 3312  
 QY 511 ValAlaHisPheArgSerleuSerHisSerCysSerIleValIlyThrIlyRlyngly 530  
 Db 3313 -----GTGAGATTCGTCCAATGATCAAGAAGTGTGACACACACGCGGAAGC 3363  
 QY 531 TrpGlucIlyValThrAsnValasnThrPropheGlyGlnPheAlaHisIaIleuLeu 550  
 Db 3364 TTCATCAGTGTGCCAACCCTTCGAC-----TTCGGCAAGTGGCGCTTCAGAGAACTAG 3417  
 QY 551 LysAsnGluGluIleLeuCysleuAlaasp----- 560  
 Db 3418 CAACACACAGCTTGAACAAAGCGCGGATTACTACGTAAACGCGACAGGAATCCGTAT 3477  
 QY 561 -----AspleuAlaThrArgleuThrGlyValTyR 570  
 Db 3478 CTGGGATTAGAAAAAGCAACCAATTTGAGCTTAACAGCGCACTGTCAACAACAAA 3537  
 QY 571 ProAlaThrAspAsnPhe-----AlaAlaIaValSer 581  
 Db 3538 TCAGCGACAGACAGCTTGGCTTACAGCGACCGCTTATTTAGGGCGCGCTGTCT 3597  
 QY 582 AlaPheAlaIaAsnMetleuSerValleuLysSerGlu-----AlaThrSerSer 599  
 Db 3598 AGCTTATACCAATATACAAATCAACCAACGAGTGAATAAATATCGGTGCTACACAGAGTGCC 3657  
 QY 600 IleIleLysSerValGlyGluThrAla 608  
 Db 3658 ATTAGCTTAACAGCCAAACACACAGCA 3684  
 RESULT 8  
 ABN98193 ID ABN98193 standard; DNA; 3840 BP.  
 AC ABN98193;  
 DE 05-AUG-2002 (first entry)  
 DE E faecalis EF108 gene.  
 KW Enterococcus; vaccine; gastrointestinal disease; diagnosis; antibiotic;  
 KW gene; ds.  
 OS Enterococcus faecalis.

XX US2002045737-A1.  
XX 18-APR-2002.  
XX 04-MAY-1998; 98US-0071035.  
XX 04-MAY-1998; 98US-0071035.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Choi GH, Bailey C, Hromocky] A, Kunsch CA;  
XX WPI: 2002-425450/45.  
XX P-PSDB: ABP43437.  
XX  
XX New genes and polypeptides from *Enterococcus faecalis*, useful as  
XX vaccines for preventing, treating or attenuating an infection caused by  
XX a member of the *Enterococcus* genus in an animal, particularly *E. faecalis*.  
XX  
XX Claim 1; Page 192-193; 255pp; English.  
XX  
XX The present invention provides the protein and coding sequences of a  
XX number of polypeptides from *Enterococcus faecalis*. The proteins can be  
XX used as vaccines for preventing or attenuating an infection caused by a  
XX member of the *Enterococcus* genus in an animal, particularly *E. faecalis*.  
XX The polynucleotide is also useful for preventing or treating *E. faecalis*  
XX infection. The present sequence is a coding sequence of the invention.  
XX  
XX Sequence 3840 BP; 1335 A; 815 C; 778 G; 912 T; 0 other;  
SQ  
Alignment Scores:  
Pred. No.: 0 138 Length: 3840  
Score: 139.50 Matches: 140  
Percent Similarity: 31.38% Conservative: 95  
Best Local Similarity: 18.69% Mismatches: 247  
Query Match: 4.13% Indels: 267  
DB: 24 Gaps: 31  
US-09-677-653a-50 (1-647) x ABN98193 (1-3840)  
QY 19 AsnValaIrgValSerIleAsnThrValThrValAsnGlyArgArgAsnGlnArgArg 38  
DB 1762 AACGCCAAGTCACCGAGAACTGCTGACACACACGCGGTAA- 1806  
QY 39 ThrGlyArgGlnValSerProProAspAsnPhetrrAlaAlaAlaGlnAspLeuAlaGln 58  
DB 1807 -ATCACACCGCCCAACAGCTTTCACCCCAAGTAAACGCGTGTACA 1854  
QY 59 SerIleuAspAlaAsnThrVal-----ThrPheProAlaAsnIleSerSer--- 73  
DB 1855 AGC--GACGGCTTACACTTTCACACAGCAGCAGCTTACAGCAGCTTACACAGCAGC 1911  
QY 74 -----MetProGluPheArgAsnTrpAlaLysGlyLysIleAspLeuAspSerAsp 91  
DB 1912 GGTAAAGACCTCAAGTCAAGGTTGTCACAAAGCAGAGTCATCTACACACATTGACA 1971  
QY 92 IleGlyTrpIlePheLysTrpLeuAspProAlaGlyAlaTrpGluSerAlaIrgAlaVal 111  
DB 1972 ACT----- 1974  
QY 112 GlyIleuTrpSerLysIleProAspIleuValLysPheSerValAspAlaGluIleArg 131  
DB 1975 -----ACCAAGCGCCCAAGTTATCAAGTACGATGACATGATGATTTGAT 2025  
QY 132 GluIleuArgAsnGluGluCysProValAlaThrAspValSerValProLeuAsp----- 149  
DB 2026 GTGGTGTATGAAGAAACAGTTACAGACATGATCATCATGATGATGATGATGATGATG 2085  
QY 150 -----GlyArgGlnTrpSerLeu 155  
DB 2086 AATGAAAAAGCGGGCTTTCACACCGGCTTAACCTTTAGTGTGTAAGTACTATCGCAA 2145

QY 156 SerIlePheSerPheProMetPheArgThrAlaTrpValAlaValAlaAsnValGluAsn 175  
DB 2146 ACTAGAGATGCGCTAC-----TTAGAACCGCATTTATATGACGTACCTCAAAAATATAT 2199  
QY 176 -----LysGluMetSerLeuAspValValAsnAspLeu 186  
DB 2200 GGTAAAGCGCATATATACGTAAGTATATATATGATGATGATGATGATGATGATGATG 2259  
QY 187 IleGlyTrpLeuAsn----- 191  
DB 2260 TTGAAAAAATATATATATATGACACCAATCAGTCTACCAACAGATTACAGTTATATGTT 2319  
QY 191 ----- 191  
DB 2320 GATAAATTAGCCATGACCAACCACTAAATATGTGACAGATTCAATTAGACACAGCT 2379  
QY 192 -----AsnLeuAlaAspTrpArgTrpValVal----- 200  
DB 2380 CAAAGTACCAATCTGAATCTATGATATGATGATGATGATGATGATGATGATGATGATG 2439  
QY 201 -----AspSerGluGlnTrpIleAsn 207  
DB 2440 GACCCAAATGACACACAGAGGTTGACCTTACCTGACAAATCTTAACCTGCTTAT 2499  
QY 208 PheThrAsnAspTrpThrTrpTrp----- 215  
DB 2500 TTTGATTCAGATGACGACCTATTTTCTAATGCAATATATACCTTTTACACGATTTA 2559  
QY 216 -----ValArgIleArgValLeuArgProThrTrpAspVal--- 227  
DB 2560 GGATATAGTGGCACACAGAGTAACTATCTCTCTGTAATGTTCTTTTAAACGCCCAA 2619  
QY 228 ProAspProThrGluGlyLeuValArgThrValSerAspTrpArgLeuThrTrpLysAla 247  
DB 2620 CCGGGGATAGTCAAACTGTC-----TACAAAGTCTGCGCAACAA 2664  
QY 248 IleThrCysGluAlaAsnMetProThrLeuValAspGlnGlyPheTrpIleGlyGlyLys 267  
DB 2665 GTACCC-----GAAACCTCGTGAT-----GTACACGCTGCC 2697  
QY 268 TyrAlaLeuThrProThrSerLeuProGlnTrpAspValSerGluAlaTyrAlaLeuHis 287  
DB 2698 AAATACCTGACCAACAGGCTTACCCAA-----GGTAACCAAGTACCAATGAC 2748  
QY 288 ThrLeuThrPheAlaArgProSerSerAlaAlaLeu----- 300  
DB 2749 AGTAACACCTTC--AACTACACAGCGCAAAAGCTTTCACAGCAGCTATACACAGT 2805  
QY 301 -----AlaPheValTrpAlaGlyLeuProGlnGlyGlyTrpAlaProAlaGlyThrPro 318  
DB 2806 GGCAAGCTTATACCTTCCAGAGGTCATTAAGGAAACCAACGCAAGTACGTTG--- 2862  
QY 319 AlaTrpGluGlnAlaSerSerGlyGlyTrpLeuThrTrpArgHisAsnGlyThrTrpPhe 338  
DB 2863 -----AACAAACAAACAACT 2877  
QY 339 ProAlaGlySerValSerTrpValLeuProGluGlyPheAlaLeuGluArgTrpAspPro 358  
DB 2878 CCAAGCTTCAATGCGCC-----TTGATGCGC 2904  
QY 359 AsnAspGlySerTrpTrpAspPheAlaSerAlaGlyAspTrpValThrPheArgGlnVal 378  
DB 2905 AATGACATATAGCCCGCATATATAGAGAAATATACCAACAGCTAGTGTACATTAAT 2964  
QY 379 AlaValAspGluValValValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPhe 398  
DB 2965 CGACCAAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3024  
QY 399 ThrValArgValProProSerAsnAlaTrpThrAsnThrValPheArgAsnThrLeuLeu 418  
DB 3025 ACTAGCAAAAGACCC-----TTACAAATCTCACCTTG 3057



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Db 4846 AGTACGAGTGGCTAC-----TTAAGACCGAGTATTATATGACGTGACCTCCAAATAATAT 4899
Oy 176 -----LysGluMetSerLeuAspValValAsnAspLeu 186
Db 4900 GGTAATGGGCAATATACGGTAAGTATTAAATGATGATGCAATGTCACCAAGAATA 4959
Oy 187 ILeuTrpLeuAsn----- 191
Db 4960 TTGAAAAATATATATATATGACACACCAATCAGTGTACCAACAGATTACAGTTATGTT 5019
Oy 191 ----- 191
Db 5020 GATAAATATGACCATGACCAACAATAAATATGTTGACAGCATTCATATAGACAGGCT 5079
Oy 192 -----AsnLeuAlaAspTrpArgTyrValVal----- 200
Db 5080 CAAAGTAGCAATCTGAAATCTATAGTATGTGTACACGACAAATAGCTCAGTGGTTTTC 5139
Oy 201 -----AspSerGluGlnTrpLeuAsn 207
Db 5140 GACCCAAATGTACACACACAGGTTGACCTTAGTTCAGAAATCTCTTAACCTTGCTTAAT 5199
Oy 208 PheTrpAsnAspTrpThrTyrTyr----- 215
Db 5200 TTGTATTCAGATGGACGACTATTTTCTAATGCAAAATATAGACTTTTACACGCAATTA 5259
Oy 216 -----ValArgIleArgValLeuArgProThrTyrAspVal--- 227
Db 5260 GGATATATGAGGACACACAGAGGATTAATCTCTCTGTAATGTTCTTTTACGCGCAA 5319
Oy 228 ProAspProThrGluGlyLeuValArgThrValSerAspTyrArgLeuThrTyrIleVal 247
Db 5320 CCTGGCGATTAAGTCAAAACTTGTCT-----TACAAAGTCACTGCGCAACAA 5364
Oy 248 ILeThrCysGluAlaAsnMetProThrLeuValAspGlnGlyPheTrpIleGlyGln 267
Db 5365 GTACACC-----GAAAACTGCGTGAAT-----GTCAACGGGTGCC 5397
Oy 268 TyrAlaLeuThrProThrSerLeuProGlnTyrAspValSerGluAlaTyrAlaLeuHis 287
Db 5398 AAAATCACTGACCAACAGCGCTTCAACCA-----GTTAACCAAGTACCACAAATGAAC 5448
Oy 288 ThrLeuThrPheAlaArgProSerSerAlaAlaLeu----- 300
Db 5449 AGTAAACACTTC---AAGTACACAGCGGCAAAAGCTTTACACGCGCATACTACAGGT 5505
Oy 301 -----AlaPheValTrpAlaGlyLeuProGlnGlyTyrAlaProAlaGlyThrPro 318
Db 5506 GGCAAAGTCTATACGTTCCAAAGGTGTATAAAGGAAACCAAGCAAGTACGTTG--- 5562
Oy 319 AlaTrpGluGlnAlaSerSerGlyGlyTyrLeuThrTrpArgHisAsnGlyThrTrpPhe 338
Db 5563 -----AACAAAAACAACAACACT 5577
Oy 339 ProAlaGlySerValSerTyrValLeuProGlnGlyPheAlaLeuGlnTyrTyrAspPro 358
Db 5578 CCAAGTTCATCGCAGC-----TTTGATGGC 5604
Oy 359 AsnAspGlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnVal 378
Db 5605 AATGACGATATGACCGCCATGTATAGGAAGAAATACCAACAGAGTGTCACTAATACT 5664
Oy 379 AlaValaAspGluValValValThrAsnAsnProAlaGlyGlySerAlaProThrPhe 398
Db 5665 CGACCAAAAGAAATGATGATACCAATGTAATCTGACACAAACGATCGAGAAAT 5724
Oy 399 ThrValArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuLeu 418
Db 5725 ACTACGAAAGCACCC-----TTCAAAATCTCACCTTG 5757
Oy 419 GluThrArgProSer---SerArgArgLeuGlnLeuPro-----MetProAlaAsp 435

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Db 5758 AAAAAAGGCCCCAATTGCTACAGTGGCTGACAGATCCGACCTTTATGGAAGTACACCA 5817
Oy 436 PheGlyGlnThrValAlaAsnAsnProLysIleGluGlnSerLeuLeuGlyGlnThrLeu 455
Db 5818 GAAGGAGAAACGACAAAATCAATCCCA---GTAAATATGACACTTTGGACAGAGGGGGTT 5874
Oy 456 GlyCysTyrLeuValHisSerLysMetArgAsnProValPheGlnLeuThrProAlaSer 475
Db 5875 -----CCTTTACCAATGCCGTTCTATCGGC 5901
Oy 476 SerPheGlyAlaValSerPhe-----AsnAsnProGlyTyrGlnArgThr 490
Db 5902 AAAAAAGTTTCAGTTCCTTCAACAACTCCGCAACAGGAAACCAACACTGTTTGA 5961
Oy 491 ArgAspLeuProAspTyrThrGlyIleArgAspSerPheAspGlnAlaMetSerThrAla 510
Db 5962 GCAAGAGTTGTAGTATTTGGTGATTAAGATAGTACAGTGGATTAACCTTC----- 6012
Oy 511 ValAlaHisPheArgSerLeuSerHisSerCysSerIleValThrLysThrTyrGlnGly 530
Db 6013 -----GTGAGAAATTCGTCCAATGATCAAGAAATGATGACACCAACGACCGAAGC 6063
Oy 531 TrpGluGlyValThrAsnValAsnThrProPheGlyGlnPheAlaHisAlaGlyLeuLeu 550
Db 6064 TTCATCAGTGTGCAACCTTCGAC-----TTCGGCAAGTGGCGGCTGCAGGAACATA 6117
Oy 551 LysAsnGluGlnLeuLeuLysLeuAlaAsp----- 560
Db 6118 CAACACACACAGCTGTAACACAGCCGGGATTAATACGCTAACGCGCACAGGAATCCGAT 6177
Oy 561 -----AspIleAlaThrArgLeuThrGlyValTyr-570
Db 6178 CTGGCGATTAAAGAAACGACCAACCAATTTGAGACTTAACGCGCACTGTCACACCAAA 6237
Oy 571 ProAlaThrAspAsnPhe-----AlaAlaAlaValSer 581
Db 6238 TCAGCGCAGACAGACTTGGCTACAGCAGCCGCTTATATTAAGGGCGCGCTGTCTCT 6297
Oy 582 AlaPheAlaAlaAsnMetLeuSerValLeuLysSerGlu-----AlaThrSerSer 599
Db 6298 AGCTTTACCAATTTACATTAACCAACCGAGTTGAAATAATAGCGTGGTACCAAGAGTGC 6357
Oy 600 IleIleLysSerValGlyGlnThrAla 608
Db 6358 ATTAGCTTAACAGCAACACACAGCA 6384

```

RESULT 10  
 ABL30182 standard; DNA: 8496 BP.  
 ABL30182;  
 26-MAR-2002 (first entry)  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42019.  
 KW Drosophila: developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ds.  
 OS Drosophila melanogaster.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PF 23-MAR-2001; 2001WO-US09231.  
 PR 23-MAR-2000; 2000US-191637F.  
 PR 11-JUL-2000; 2000US-0614150.  
 PA (PEKE ) PE CORP NY.  
 PI Venter JC, Adams M, Li PWD, Myers EW;

XX WIPI; 2001-656860/75.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from *Drosophila* and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Claim 1: SEQ ID NO 42019; 21bp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from *Drosophila*. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB101840-AB16175) and the encoded proteins  
 CC sequences (AB101840-AB16175) and the encoded proteins  
 CC (AB16175-AB16175).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SO Sequence 8496 BP; 2467 A; 1839 C; 1860 G; 2330 T; 0 other:  
 XX  
 Alignment Scores:  
 Pred. No.: 2.37 Length: 8496  
 Score: 130.50 Matches: 148  
 Percent Similarity: 31.13% Conservative: 73  
 Best Local Similarity: 20.85% Mismatches: 256  
 Query Match: 3.87% Indels: 233  
 DB: 23 Gaps: 36  
 US-09-677-653a-50 (1-647) x ABL30182 (1-8496)  
 QY 70 AsnIleSerSerMetProGluPheArgAsnTrpAlaIleGlySerIleAspLeuAspSer 89  
 DB |||:||||| ||| ||| |||:|||||  
 DB 4593 AACGTACACCTTAAGCCCACTTCCCTACTCTCCATGGTGGTG----- 4640  
 QY 90 AspSerIleGlyTrpTyrrPheIleAspLeuProAlaGlyAla-----ThrGlu 106  
 DB ||| ||| |||:||||| ||| ||| |||:|||||  
 DB 4641 -----TACTTCTACTAGCTGGATGACAGAGAGGTTCCGATATACCGAG 4685  
 QY 107 SerAlaArgAlaValGlyGluTyrrSerIleProAspGlyLeuValIlePheSerVal 126  
 DB 4686 GAAACA-----TTACGTTGTG 4700  
 QY 127 AspAlaIleuIleArgGluIleTyrrAsnGluIleCysProValValThrAspValSerVal 146  
 DB |||:||||| ||| ||| |||:|||||  
 DB 4701 GAGGTGAGCTGCAAGAACGATCGAATCAAGCTCCCGGGAAGTTAA----- 4751  
 QY 147 ProLeuAspGlyArgGluIleTrpSerIlePheSerPheProMetPheArgThrAla 166  
 DB ||| ||| |||:||||| ||| ||| |||:|||||  
 DB 4752 -----CCGGTCCCGACGTTGGCACTGGAGATCAAGACGTCGCA-----AAGTCA 4796  
 QY 167 TyrrValAlaValAlaAsnValGluAsnIleGluMetSerLeuAspValValAsnAspLeu 186  
 DB ||| ||| |||:||||| ||| ||| |||:|||||  
 DB 4797 TTGCTTGATTTGGTGGCGGATGATGATGCTCTCTGCTGGGACAGCAACAGATTTG 4856  
 QY 187 -----IleGluTrpLeuAsnAsnLeuAlaAspTrpArgTyrrValValAspSer 202  
 DB 4857 AACAGGAATCTTCAACTGGCGCTAAATGGCTATGAC-----ACCTCA 4901  
 QY 203 GluIleTrpIleAsnPheTrpAsnAspThrThrTyrrTyrrValAlaGlyIleArgValLeuArg 222  
 DB 4902 ACTCCCTGG-----CAGGTGATCTCTACTATAC----- 4931  
 QY 223 ProThrTyrrAspValProAspProThrGluIleValVal----- 235  
 DB 4932 -----CCCGAGAGAGCACTGGAGTCTGACTATGACCAATGCTATTTC 4976  
 QY 236 -----ArgThrValSerAspTyrrArgLeu--ThrTyrrIys-----AlaIleThr 249  
 DB 4977 TTCTATATGCAACCGCCCACTCAATATTCGTACATATAATTGTTCATATATAATA 5036

QY 250 CysGluAlaAsnMetProThrLeu---ValAspGlnIleGlySerIleGlyGluIleTyrr 268  
 DB |||:||||| ||| ||| |||:|||||  
 DB 5037 AACCACTTAATTTGGCAATTAATTTGGAGTTAGACAGAGATTGGT---GGAAGCTTTTC 5093  
 QY 269 AlaLeuThrProThrSerLeuProGluIleTyrrAspValSerGluAlaIleuIleThr 288  
 DB ||| ||| |||:||||| ||| ||| |||:|||||  
 DB 5094 GCCATGAGAAAGACTACAGTG-----GCACATGATGATCATTTTCATTTCC 5141  
 QY 289 -----LeuThrPheAlaArgProSerSerAlaAlaLeu 300  
 DB 5142 GTTGCTGGCGGACCACTGACGGCGTGGGATTTCCCGCAAAAGTGGTGCATTCGA 5201  
 QY 301 Ala----- 301  
 DB 5202 GCACCACTAGTGCAGAAAGATTTCGACAGACCTGATCTTGGCATTCAGAGACACC 5261  
 QY 302 -----PheValIleProAlaGlyLeuProGlnIleGlyThrAlaProAlaGlyThr 317  
 DB 5262 GAGGAGGAGGTGTCAAGTGGGA-----AAGACCATACCGATACGATC 5306  
 QY 318 ProAlaTrp-----GluIleAlaSerSerGlyIleTyrrLeuThr 330  
 DB 5307 ACCAATGGGTGGTGCACCGGCTTTTCACTGCATCCCAAGAGGATTAGGTCCACCAAT 5366  
 QY 331 TrpArgHisAsnGlyThrThrPheProAlaGlySerValSerTyrrValLeuProGluGly 350  
 DB ||| ||| |||:||||| ||| ||| |||:|||||  
 DB 5367 GATCAGACAAATATACAGACATTCACCGCTTCTTCTGTCGTCGATTCGCA----- 5420  
 QY 351 PheAlaLeuGluArg-----TyrrAspPro 358  
 DB 5421 TACTCCGTGAAGCGAGGTGATGATCATATGATACCGGACACTGCTTAACTACTCCGCC 5480  
 QY 359 -----AsnAspIleSerTrpThrAspPheAlaSer 368  
 DB 5481 AAGACACTGACGTGACATGACCTGACCTGACACAGGATGACAGATATCTGTGGAT 5540  
 QY 369 AlaGlyAspThrValIleThrPheArgGluValAlaValAspGluValIleThrAsnAsn 388  
 DB ||| ||| |||:||||| ||| ||| |||:|||||  
 DB 5541 GCCTCGAATGAGTTATTTGGTGACACAGACGTCACGAAACATCAAGTGGGCCCAAC 5600  
 QY 389 ProAlaGlyGlySerAlaProThrPheThrValArg----- 401  
 DB 5601 GAGCGGACAGAGCCTCA-----TTTGTATCCGACCAAGTCATTTGAATATTT 5651  
 QY 401 ----- 401  
 DB 5652 TTGCTGAATTAAGGCCATCTACCGCTGCGGAGATGCTATACAAAGCCGTTAAG 5711  
 QY 402 ---ValProProSer---AsnAlaTyrrThrAsnThrValPheArgAsnThrLeuGlu 419  
 DB ||| ||| |||:||||| ||| ||| |||:|||||  
 DB 5712 GTAGTGGCCGAGGAATTTACCACTGACAGACAGGCGATTTTATCAATCTTAAGAT 5771  
 QY 420 ThrArgProSerSerArgArgLeuGluLeuProMetProProAlaAspPheGlyIleThr 439  
 DB ||| ||| |||:||||| ||| ||| |||:|||||  
 DB 5772 ACGGTGATTTAGAACACCTTGACCTGGAAGTCCGAG-----GATGTG 5819  
 QY 440 ValAlaAsnAsnProIleGlu----- 447  
 DB 5820 GTCCCCGACCTCCGAGCGCTGGGAATTCGATTCGGGTGATCTCTTGGGACAGTGTGC 5879  
 QY 448 -----GlnSerLeuLeuGlyIleThrLeuGlyIys----- 457  
 DB 5880 AAGAACCTTAGAACCTGTGGCGTTGCCAGCGGTGGCGGTGAGCAACCAATGTCCAA 5939  
 QY 458 -----TyrrLeuValHisSerIleMetArgAsnProValPheGlnLeuPro 473  
 DB 5940 TTGGTGCCCAACATATCTGGTGGAGGATTAATCTGAAGAC---ATCAAGAAATCAACCT 5996  
 QY 474 AlaSerSerPheGlyAlaValSerPheAsnAsnProGlyTyrrGluArgThrArgAspLeu 493  
 DB 5997 GCATTGGACACTGCATCAAGAGGAATCTGCAGACGATACCAACATATATGTTGCACTAT 6056  
 QY 494 ProAspTyrrThrGlyIleArgAspSerPheAsp----- 504







DR WPI: 2001-656860/75.

XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -

PS Claim 1: SEQ ID NO 9118; 21bp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (AB101840-AB16175), expressed DNA  
CC sequences (AB101840-AB16175) and the encoded proteins  
CC (AB57737-AB872072).

CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [ftp.wipo.int/pub/publicated\\_pcl\\_sequences](http://pub.int/pub/publicated_pcl_sequences).

XX Sequence 6592 BP; 1705 A; 1969 C; 1673 G; 1245 T; 0 other:

Alignment Scores:  
Pred. No.: 3.29 Length: 6592  
Score: 127.00 Matches: 77  
Percent Similarity: 32.80% Conservative: 45  
Best Local Similarity: 20.70% Mismatches: 116  
Query Match: 3.76% Indels: 134  
DB: 23 Gaps: 18

US-09-677-653a-50 (1-647) x ABL19215 (1-6592)

QY 231 ThrGluGlyLeuValArgThrValSerAspTyrArgLeuThrTyrLysAlaIleThrCys 250  
DB 4294 ACTGAGACAAAGACCAGAGGTTCCCACTACAGATGAGTTTCAGGCGACCGAAGC 4353  
QY 251 GluAlaAsnMetCysProThrLeuValAspGlnGlyPheTrpIle----- 264  
DB 4354 GAGAGAACACAGCC-----TACGAGTTCTGGGTGATGACACCTAGCACCACTATT 4401  
QY 265 ---GlyGlyGlnTyrAlaLeuThrProThrSerLeuProGlnTyrAspAlaSerGluAla 283  
DB 4402 GCGGAGGCCGACGACGATGAGCATAGTGGCCATGCCAGGACCGACCGCCGCGCAAG 4461  
QY 284 TyrAla-----LeuHisThrLeuThrPheAlaArgProSerSerAlaAla 299  
DB 4462 ATCGCCTCTTGGACGACACCTTCACTGCCACTTCAAGAGAGCGCCAAAGATGCCCTGC 4521  
QY 300 LeuAlaPheValTyrPalaGlyLeuProGlnGlyTyrAlaProAlaGlyThrProAla 319  
DB 4522 CTGGCC-----GTTGAGACCCCCCAA----- 4542  
QY 320 TrpGluGlnAlaSerSerGlyTyrLeuThrTyrPargHisAsnGlyThrThrPhePro 339  
DB 4543 -----CCGAGATCATGATGAGATCAAGGCGCTCGAATTCACT 4581  
QY 340 AlaGlySerValSerTyrValLeuProGlnGlyPheAlaLeu-----GluArg 355  
DB 4582 GCCAAGATCGATCGCGCTCTCTCCCGACGATGCTCTATCAAGTCGGTAATCC 4641  
QY 356 TyrAspProAsnAspGlySer---TrpThrAspPheAlaSerAlaGlyAspThrValThr 374  
DB 4642 CAGGATGGCGGAGAGACTCTGCGACGCGGAGAACTGATTCGTAAGACATCATCAG 4701  
QY 375 PheArgGlnValAlaVal----- 380  
DB 4702 CACAAACTGATGTCTGCGACACACACAAATCGCCCAAGTCACCTTCGCGAAACACC 4761  
QY 381 ---AspGluValValValThrAsnAsnProAlaGlyGlySerAlaProThr----- 397  
DB 4762 ACTGATGCCCTGACTGATTAAGTTGAAGCCCATGAGGGGAGACATGCTCTCTGATGGA 4821  
QY 398 PheThrValArgValProProser----- 405

DB 4822 TACACCTGCTACTACAGCCAGAAATTCGAGATGGGAACATCGGAAGTGTCTGTGAC 4881  
QY 406 -----AsnAlaTyrThrAsn 410  
DB 4882 TCACAGACACACATCGAAGGCTCTTGTGGCGCTCCCGCTATGAGCTTATGCC---- 4938  
QY 411 ThrValPheArgAsn-----ThrLeuGlnThrArgProSer 423  
DB 4939 ACAGGATTCATATACATTGGAGCTGGCGAAGCTTTCAGACATTTTGAACACCGGACCAAG 4998  
QY 424 SerArgArgLeuGluLeuProMetProProAlaAspPheGlyGlnThrValAlaAsnAsn 443  
DB 4999 GGACAGAACCCCAAGCTGCCCGGAGAAACCTCGC---TTCATTGAAGTGTGTCAACTCG 5055  
QY 444 ProlYsIleGlnGlnSerLeuLeuLysGluThrLeuGlyCys-----TyrLeu 459  
DB 5056 GTGTCCCTGCTACTTCAAGGCTGGAAAGATGGA---GGATGCCCATGTGCGACTTTGTG 5112  
QY 460 ValHisSerLysMetArgAsnPro----- 467  
DB 5113 GTGAGACGACAGAAAGCGCATCAATTTGATGGAAACCAATTTGAAACAGTGAAGCCC 5172  
QY 468 -----ValPheGlnLeuThrProAlaSerSerPheGly-----AlaVal 480  
DB 5173 GATTAACACTAGCTGTGTTTGGACCTGGAACCCGCGCATGTTCAACCTCGCATCACT 5232  
QY 481 SerPheAsnAsnProGlyTyr----- 487  
DB 5233 GCCCACAACCTGGCTGGCTTCACTGTGCGCGAATACGACTTTGCCACTTAACCTTACC 5292  
QY 488 -----GluArgThrArgAspLeuProAsp 495  
DB 5293 GGAGGCATATCGCACCTCGCGAGATTTTACCGGAG 5328  
RESULT 13  
AAS31116  
ID AAS31116 standard; cDNA; 8277 BP.  
XX  
AC AAS31116;  
DT 04-DEC-2001 (first entry)  
XX  
DE Human diagnostic and therapeutic polynucleotide (DITHP) #131.  
KW Human; receptor; diagnostic; therapeutic; gene therapy; vaccine;  
KW cell proliferative disorder; Crohn's disease; lymphoma; leukaemia;  
KW acquired immune deficiency syndrome; AIDS; autoimmune disorder;  
KW respiratory disorder; ss.  
OS Homo sapiens.  
XX  
PN WO200162927-A2.  
PD 30-AUG-2001.  
XX  
XX 21-FEB-2001; 2001WO-US06059.  
PF  
XX  
PR 24-FEB-2000; 2000US-0184693.  
PR 24-FEB-2000; 2000US-0184697.  
PR 24-FEB-2000; 2000US-0184698.  
PR 24-FEB-2000; 2000US-0184768.  
PR 24-FEB-2000; 2000US-0184769.  
PR 24-FEB-2000; 2000US-0184770.  
PR 24-FEB-2000; 2000US-0184771.  
PR 24-FEB-2000; 2000US-0184772.  
PR 24-FEB-2000; 2000US-0184773.  
PR 24-FEB-2000; 2000US-0184774.  
PR 24-FEB-2000; 2000US-0184776.  
PR 24-FEB-2000; 2000US-0184777.  
PR 24-FEB-2000; 2000US-0184797.  
PR 24-FEB-2000; 2000US-0184813.  
PR 24-FEB-2000; 2000US-0184837.

PR 24-FEB-2000: 2000US-0184841.  
 PR 24-FEB-2000: 2000US-0185213.  
 PR 24-FEB-2000: 2000US-0185216.  
 PR 12-MAY-2000: 2000US-0203785.  
 PR 15-MAY-2000: 2000US-0204226.  
 PR 16-MAY-2000: 2000US-0204525.  
 PR 16-MAY-2000: 2000US-0204821.  
 PR 16-MAY-2000: 2000US-0204908.  
 PR 16-MAY-2000: 2000US-0205232.  
 PR 17-MAY-2000: 2000US-0204815.  
 PR 17-MAY-2000: 2000US-0204863.  
 PR 17-MAY-2000: 2000US-0205221.  
 PR 17-MAY-2000: 2000US-0205285.  
 PR 17-MAY-2000: 2000US-0205286.  
 PR 17-MAY-2000: 2000US-0205287.  
 PR 17-MAY-2000: 2000US-0205323.  
 PR 17-MAY-2000: 2000US-0205324.  
 XX  
 XX (INCYTE GENOMICS INC.)

PI Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC;  
 PI Chen A, D'Sa SA, Amshy S, Dahl CR, Dam TC, Daniels SE;  
 PI Dufour GE, Flores V, Fong WT, Greenwalt LB, Hillman JL, Jones AL;  
 PI Liu TF, Roseberry AM, Rosen BH, Russo FD, Stockreher TK, Daffio A;  
 PI Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W;  
 PI Cohen HT, Hodgson DM, Lincoln SE, Jackson S;  
 XX  
 DR WPI: 2001-502867/55.  
 DR P-PSDB: AA019545.

PT Polynucleotides encoding diagnostic and therapeutic proteins, e.g.  
 PT enzymes, hormones and receptors, useful in diagnostics and therapeutics

XX Claim 1: Page 356-358; 522pp; English.

XX The invention relates to polynucleotides (I) encoding diagnostic and  
 CC therapeutic (DITHP) polypeptides (II), which include e.g. enzymes,  
 CC and proteins involved in growth and development and receptors. (I) and  
 CC (II) may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate DITHP expression. For example, (I) and  
 CC (II) may be used to treat disorders associated with decreased polypeptide  
 CC expression by rectifying mutations or deletions in a patient's genome,  
 CC that affect the activity of the DITHPs, by expressing inactive proteins  
 CC or supplementing the patient's own production of them. (I) and (II)  
 CC may be used to treat diseases, for example, cell proliferative disorder,  
 CC Crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma,  
 CC leukemia, autoimmune disorders, and respiratory disorders. Additionally,  
 CC (I) may be used to produce the DITHPs, by inserting the nucleic acids  
 CC into a host cell and culturing the cell to express the protein. (I) and  
 CC its complementary sequences may also be used as DNA probes in diagnostic  
 CC assays to detect and quantitate the presence of similar nucleic acids in  
 CC samples, and therefore which patients may be in need of restorative  
 CC therapy. (II) may also be used as antigens in the production of  
 CC antibodies against DITHPs and in assays to identify modulators of DITHP  
 CC expression and activity. The anti-DITHP antibodies and antagonists may  
 CC also be used to down regulate expression and activity. The anti-DITHP  
 CC antibodies may also be used as diagnostic agents for detecting the  
 CC presence of DITHPs in samples (e.g. by enzyme linked immunosorbant  
 CC assay (ELISA)). AAS30986-AAS31196 represent human diagnostic and  
 CC therapeutic (DITHP) polynucleotides of the invention.

XX SO Sequence 8277 BP; 2316 A; 1962 C; 1890 G; 2106 T; 3 other;

Alignment Scores:

Pred. No.: 4.96 Length: 8277  
 Score: 126.50 Matches: 133  
 Percent Similarity: 34.87% Conservative: 71  
 Best Local Similarity: 22.74% Mismatches: 186  
 Query Match: 3.75% Indels: 195  
 DB: 22 Gaps: 33

US-09-677-653A-50 (1-647) x AAS31116 (1-8277)

QY 12 HisAsnArgArgGlyThrArgAsnValArgValSerAlaAsn-ThrValThrValAsnG1 31  
 ||||| : : : : : ||||| |||  
 DB 997 CACAATGCCAAGTCCAGCTGTCCCTGAGGTGTTCGCAAGCA----- 1042  
 QY 31 YArgArgAsnGln-----ArgArgArgThrGlyArgGlnValSerProAs 47  
 ||||| : : : : : ||||| |||  
 DB 1043 -AGGAGATCTGCATGATCAAGGTAGAGATCCAGCACTCAACGACAGCGCCCTCCTTC 1101  
 QY 47 PAsnPheThrAlaAlaAlaGlnAspLeuAlaGlnSerLeu----- 60  
 ||||| : : : : : ||||| |||  
 DB 1102 TCCTCGGACCAAGATCAAGATGACATCTCGAGAACCTGTCCGCGGACCCGCTCC 1161  
 QY 61 ----AspAlaAsnThrValThrPheProAlaAsnIleSerSerMetProGluPheArg 79  
 ||||| : : : : : ||||| |||  
 DB 1162 CTCACCGACGCGACATGACCCCGACCGAGAGATGGCTCCGACCT-----AC 1212  
 QY 79 nTrpAlaLysGlyLysIleAspLeuAspSerAspSerIleGlyTrpTrpPheLysTyrLe 99  
 : : : : : ||||| |||  
 DB 1213 CTGCTCAGCGCGACGATC-----ACGGCTCTTTGGACTGGACGTTAAGTCAGC 1263  
 QY 99 uAspProAlaGlyAlaThrGlnSerAlaArgAlaValGlyLysSerLysIleProAs 119  
 ||||| : : : : : ||||| |||  
 DB 1264 GCGCAGCGCA-----CCAGAGTTCACGA 1287  
 QY 119 pGlyLeuValLysPheSerValAspAlaGluIleArgGluIleTyrAsnGluLysP 139  
 : : : : : ||||| |||  
 DB 1288 ACTGCTATCCAGAGAGCTGTGC-----CGGACCAACAGATCAACATACGCT 1338  
 QY 139 oValValThrAspValSerValProLeuAspGlyArgGlnTrpSerLeuSerIlePheSe 159  
 ||||| : : : : : ||||| |||  
 DB 1339 GTCCTGACT-----GCCCTGACGCTGGCAG----- 1366  
 QY 159 rPheProMetPheArgThrAlaTyrValAlaValAlaAsnValGlnAsnLysGluMetSe 179  
 ||||| : : : : : ||||| |||  
 DB 1367 -CTCCAGCTTCGCCCGCACCGACAGATCAACGATGATGATCAACGACAG 1425  
 QY 179 r-----LeuAspValValAsnAspLeuIleGluTrpLeuAsnLeuAlaAspTrpAr 197  
 ||||| : : : : : ||||| |||  
 DB 1426 CCGCGTTCGAGCGCCATCTGATGGGAACTCCCGAGAACCTCCGCTGGGTAC 1485  
 QY 197 gTyrValValAspSerGlnGlnTrpIleAsnPheThrAsn----- 210  
 ||||| : : : : : ||||| |||  
 DB 1486 AGTGTATATGAT-----CTGAGCGCACCGGCGCATGAGTCCCATG 1533  
 QY 211 -AspThrThrTyr-----TyrValArgIleArgValLeuArgProThrTyrAs 226  
 : : : : : ||||| |||  
 DB 1534 TGAAGTCTCTACTCTTTCAGACAGCTACGTGCTGACCGCTG-----CGGAGCTCTTCTC 1590  
 QY 226 pValProAspProThrGlnGluGlyLeuValArgThrValSer-----AspTyr 241  
 : : : : : ||||| |||  
 DB 1591 CACC--GACCCCAAGACCGGCTTAATCCGTGACAGCGCAATCTGAGTATGAGAA 1647  
 : : : : : ||||| |||  
 QY 241 ----- 241  
 DB 1648 CGGATCTGAGATTCAGTTCAGCGCGGCGGAGACTTGGGCGCTTAATCCAGCCA 1707  
 QY 242 ----ArgLeuThrTyrLysAlaIleThrCysGluAlaAsnMetProThrLeuValAspG1 260  
 : : : : : ||||| |||  
 DB 1708 CTCGAAGTCAAGGTCAAGTCAATCGACCGACCAAGCAATGCGCGCTCAATC----- 1759  
 QY 260 nGlyPheTrpIleGlyGlnGlyTrpAlaLeuThrProThrSerLeuProGlnTyrAspVa 280  
 ||||| : : : : : ||||| |||  
 DB 1760 -GGTTC-----GTCTCGTCCGCGCAAGGGGGCGCT 1788  
 QY 280 lSerGluAlaTyrAlaLeuHisThrLeuThrPheAlaArgProSerSerAlaAlaAlaLe 300  
 : : : : : ||||| |||  
 DB 1789 GAGCGAGGCG-----GCCCTCCCGGCGACCGTCAATCGGCT 1824  
 QY 300 uAlaPheValTrp-----AlaGly-----LeuPr 308  
 ||||| : : : : : ||||| |||  
 DB 1825 GGTGCGGTCACTGACCGGAGCTGTGCAAGACGACAGCTGACGTGCTGCTTAGG 1884

QY 308 oGInGlyGlyThrAlaProAlaGlyThrProAlaTrrGluAlaSerSerGlyGly 328  
 |||||  
 Db 1885 CGGAGGAGGAGCGCGCGCGCGG----- 1909  
 QY 328 rleuThrTrpArgHisAsnGlyThrThrProAlaGlySerValSerTyValleuPr 348  
 |||||  
 Db 1910 -----GGCTGGGCGGCGCGGCGGCTTCCCTCAAGCTGA 1950  
 QY 348 oGluGlyPheAlaLeuGluArgTyAspProAsnAspGlySerTrpThrPheAlaSe 368  
 |||||  
 Db 1951 GGAGACTAC-----GACACTTCTACAG----- 1975  
 QY 368 rAlaGlyAspThrValThrPheArgGlnVal-----AlaValAspGluValValVa 385  
 |||||  
 Db 1976 -----GTGTGACTGACCGCGCGGATGGACCGGAGACACAGACATGACATCA 2025  
 QY 385 lThrAsnAsnProAlaGlyGlyGlySerAlaPro-----ThrPheThrVa 400  
 |||||  
 Db 2026 GACCATCGTGGCGCGGAGCGGCGCTCTCCCTCAACTCCACCAAGTCGTTGCGGAT 2085  
 QY 400 lArgVal-----ProPro-SerAsnAlaTyThrAsnThrValPhea 414  
 |||||  
 Db 2086 CAAGATTCTAGACAGACAGACACACCGCTGCTCACCAAGGCTCTAGCTGCTTCA 2145  
 QY 414 rGAsnThrLeuLeuGluThrArgProSerSerArgArgLeuGluLeuProMetProPro 434  
 |||||  
 Db 2146 GGGCGCAGAGAACACATCCCGGAGAGATCGGCGCTGTGCTGCGCAGGATCCG- 2204  
 QY 434 lAspPheGlyGlnThrValAlaAsnAsnProGlySileGluGlnSerLeuLeuGlyGluT 454  
 |||||  
 Db 2205 -----ACCTGGGCGCAGACAGACGCGACCGCTATCTACTATCTGCGCTCGC 2250  
 QY 454 hrlEuGlyCysTyrlLeuValHisSerLysMetArg--AsnProValPheGlnLeuThrP 473  
 |||||  
 Db 2251 ACATGCGGACGAGTGTATCTACACTATGCTGTGATCC-----ACGA 2298  
 QY 473 rAlaSerSerPheGlyAlaValSerPheAsnAsnProGlyTyrlGluArgThrArgAspI 493  
 |||||  
 Db 2299 ACGGCGCATCTACCGCTCGCTCTTAC-----TTCGAGCAGACCAAGCGCTT 2349  
 QY 493 euProAspTyrlThrGlylleArgAspSerPheAspGlnAsnMetSerThrAlaValAlaH 513  
 |||||  
 Db 2350 TTGAGTCTCAAGTCTTGTCTAAGAC-----TCGGGGCGCGCGCGC 2391  
 QY 513 lAspPheArgSer 516  
 |||||  
 Db 2392 ACTTGGAGAGC 2402  
 RESULT 14  
 ABQ90255 standard; DNA; 1548 BP.  
 XX ABQ90255;  
 AC ABQ90255;  
 XX 01-OCT-2002 (first entry)  
 XX DE M. capsulatus gene #240 for DNA array.  
 XX DE M. capsulatus gene; ds; differential expression; gene expression.  
 XX OS Methylococcus capsulatus.  
 XX PN WO200255655-A2.  
 XX PD 18-JUL-2002.  
 XX PF 14-JAN-2002; 2002WO-NO00019.  
 XX PR 12-JAN-2001; 2001NO-0000235.  
 XX PR 12-JAN-2001; 2001NO-0000235.  
 XX PA (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.  
 PA (TIGR-) TIGR.

XX Birkeland NK, Eldhammer I, Jonassen I, Jensen HB, Lien T;  
 PI Lillehaug JR, Lossius I, Eisen JA, Fraser CW, Durkin AS;  
 PI Salberg SL;  
 XX WPI: 2002-557818/59.  
 XX Novel DNA array useful for determining differential expression of  
 PT Methylococcus capsulatus genes, comprises polynucleotides or  
 PT oligonucleotides representative for a selective number of Methylococcus  
 PT capsulatus genes  
 XX  
 PS Claim 19: Page 166; 67bpb; English.  
 XX  
 CC The invention relates to a novel DNA array giving a representation of a  
 CC number of Methylococcus capsulatus genes. The method of the invention is  
 CC useful for determination of the differential expression of the genes of  
 CC M. capsulatus, and for studying gene expression on a genomic scale and in  
 CC gene expression assays of M. capsulatus genes. The sequences shown in  
 CC ABQ9016-ABQ91855 represent M. capsulatus genes for use in arrays of the  
 CC invention.  
 XX  
 SO Sequence 1548 BP; 231 A; 531 C; 457 G; 329 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 0.543 Length: 1548  
 Score: 126.00 Matches: 127  
 Percent Similarity: 32.15% Conservative: 64  
 Best Local Similarity: 21.38% Mismatches: 187  
 Query Match: 3.73% Indels: 218  
 DB: 24 Gaps: 31  
 US-09-677-653a-50 (1-647) x ABQ90255 (1-1548)  
 QY 141 ValThrAspVal---SerValProLeuAspGlyArgGlnTrpSerLeuSerIlePheSer 159  
 |||||  
 Db 1 ATGACCGAGATCGAGACATCCCTTC-----CCGCGCTG-----ATCGGCTTT 45  
 QY 160 PheProMetPheArgThrAlaTyrlAlaValAlaAsnValGluAsnLysGluMetSer 179  
 |||||  
 Db 46 TTCGGATGTGTGTGGAGATCTTTCATGCGGATCTTGACATCCAGATCGTCCGCACTTG 105  
 QY 180 LeuAspValVal-----AsnAspLeuIleGluTrpLeuAsnAsn 192  
 |||||  
 Db 106 CTGAGACAGATCCAGCGCGCTCGCGCCACCGGAGAGATTAATCAGGGGAGAC 165  
 QY 193 -----LeuAlaAspTrpArgTyrlValAlaAspSerGluGlnTrpIleAsnPheThrAsn 210  
 |||||  
 Db 166 GCTTACCTGATCGCGGACAGTGTGTCATCCGCTGTCGGGTGGCTGAACCGCGCCCTC 225  
 QY 211 AspThrThrTyrlValArgIleArgValLeuArgProThrTyrlAspValProAspPro 230  
 |||||  
 Db 226 TCGACCGCTTACTG----- 240  
 QY 231 ThrGluGlyLeuValArgThrValSerAspTyrlArgLeuThrTyrlValIleThrCys 250  
 |||||  
 Db 241 -----TTCGTGCGCTGCGCGCGCTTACCTTACCCAGCCGTCGCGCGCTG 291  
 QY 251 GluAlaAsnMetProThrLeuValAsp-----GlnGlyPheTrpIleGlyGly 266  
 |||||  
 Db 292 GCGTGAACCTCCCTCGATGATCGCGTTCGCGGCGCTGCTTCTTC---GGCGGG 348  
 QY 267 GlnTyrlAlaLeuThrProThrSerLeuProGlnTyrlAspValSerGluAlaTyrlAlaLeu 286  
 |||||  
 Db 349 -----GCCATGATCCGACGCTATTCGG-----GTGATT 378  
 QY 287 HisThrLeuThrPheAlaArgProSerSerAlaAlaAlaLeuAlaPheValTrpAlaGly 306  
 |||||  
 Db 379 TACACCTGTTC-----CCGCGCGCGCAGCAGGACCATGATCGTGTGCGC 429  
 QY 307 LeuProGlnGlyGlyThrAlaProAlaGlyThrProAlaTrpGluAlaSerGly 326  
 |||||  
 Db 430 CTGTGTGTG---ACGGTGGCGCCACCGCGCGCGCTG-----CTCGGC 471

```

QY 327 GYTYRLeuThr-----TrpArgHis----- 333
    |||||
Db 472 GGGTATCTGACGAAAGCTCTGCTGTGAAAGGCCCTCTTCTGTCAATCTGTCGGGGC 531
QY 333 ----- 333
Db 532 GTGCTGGCCCTTTCGACCTGTCTCTGTGGAGGTAGACCAAGCCGGAATGAGACCTG 591
QY 334 ---AsnGlyThrThrPheProAla-----GlySerValSer 344
    |||||
Db 592 CTCGAAGCGGTGATTTTCCGGCATCTCTACATCGCGCTTTTTCGGGACAGCTCCAA 651
QY 345 TyrValLeuProGluGlyPheAlaLeuGluArgTyrAspProAsnAspGlySerTyrThr 364
    |||||
Db 652 TTGCTCTGGAGAAAGGATCCGCGAGAAATGTTGATTCAGCCGAGATGTTCTTC 711
QY 365 AspPheAlaSer-----AlaGlyAspThrValThrPheArgGlnValAlaValAspGlu 382
    |||||
Db 712 AGGCGCGTGGGTATGCGCGGCGGCGCATTTCTACCGGACGCTGCCATCGAGGAA 771
QY 383 ValValVal-----ThrAsnAsnProAlaGlyGlySerAlaProThr 397
    |||||
Db 772 CCCATGCTGACCTGTGGGCTTCGCTAACACCAATTTGCGGGTCCGCTGCTGCAGC 831
QY 398 PheThrValArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeu 417
    |||||
Db 832 TTCATCATCGCGCAVC-----GGGCTCTATACCTCATCGCGTTGAGCCGCTCTAC 882
QY 418 LeuGluThrArgProSerSerArgLeuGluLeuProMetProProAlaAspPheGly 437
    |||||
Db 883 CTTCACAGCGTGAAGGCCCAACACCTGCAG----- 915
QY 438 GlnThrValAlaAlaAsnAsnProLysIleGluGlnSerLeuLeuGlyCys 457
    |||||
Db 916 -----ATCGGGCAG 924
QY 458 TyrLeuValHisSerLysMetArgAsnProValPheGlnLeuThrProAlaSerSerPhe 477
    |||||
Db 925 TACCTATGTGTACCGCGCATG-----TTCAGATTC-----GCCCTGGCTTTC 966
QY 478 GlyAlaValSerPheAsnAsnProGlyTyrGluArgThrArgAspLeuProAspTyrThr 497
    |||||
Db 967 GTGGCG-----GGACCTTGCGGAACGG----- 990
QY 498 GlyIleArgAspSerPheAsnAsnMetSerThrAlaValAlaHisPhe----- 514
    |||||
Db 991 -----ATGGACTGCGCTGTGATGTGGCGCTGCGCTCTCTTCGGA 1035
QY 515 -----ArgSerLeuSerHisSerCysSerIleValThrLysThrTyr 528
    |||||
Db 1036 CTGGGCTCATGCTGAACGGAAGCTGAGCCACGAC----- 1071
QY 529 GlnGlyTyrPheGluVal-----ThrAsnValAsn 538
    |||||
Db 1072 TTCGGCTACAG--GGAATTTCTGGGGCCAGCCCTGCGGGCTTGCCCTGATGTTCCG 1130
QY 539 ThrProPheGlyGlnPheAlaHisAla--GlyLeuLeuLysAsnGlnGluIleLeuCysIle 558
    |||||
Db 1131 CTTCCTGCGCCATCAATTCGTGGCTGGGAACCTGCCACAGAGAGAGCTC----- 1182
QY 558 uAlaAspAspLeuAlaThrArgLeuThrGlyValTyrProAlaThrAspAsnPheAlaAl 578
    |||||
Db 1183 -----AAGAAATGCCAGCGGGCTGTACAACTCACCAGCGCATCTGGGCGG 1226
QY 578 aAlaValSerAlaPheAlaAlaAsnMetLeuSer-----Se 590
    |||||
Db 1227 CGCGATCGGATCGCGGTGCGCAATCCGTGATGATCCGTGGGACAAAGCATTAACGC 1286
QY 590 rValLeuLysSerGluAlaThrSerSerIleIleLysSerValGlyGluThrAlaValG 610
    |||||
Db 1287 CGCGCTGCGGATTCGCTACAGCC--GGTTTC-----TCCACAGCGCGACGCGCTCTGTA 1339

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```

QY 610 yAlaAlaGlnSerGlyLeuAlaLysLeuProGlyLeuLeuMetSerValProGlyLysI 630
    |||||
Db 1340 CGCGGCTGGAAGC-----CCAAGCGCGCC 1363
QY 630 eAlaAlaArgValArgAlaArgAlaArgAlaArgAla 643
    |||||
Db 1364 TGCTCCGCGTCTCGATCCGCGCGGACGCCGCACTCAAGCA 1403

RESULT 15
AAx81820
ID AAx81820 standard; cDNA; 2748 BP.
XX
AC AAx81820;
XX
DT 02-SEP-1999 (first entry)
XX
DE Talaromyces emersonii glucoamylase enzyme gene locus.
XX
KW Glucoamylase enzyme; saccharification; starch hydrolyzate;
KW dextrose syrup; syrup; ethanol; fuel; beverage; citric acid;
KW ascorbic acid; lysine; glutamic acid; ss.
XX
Talaromyces emersonii.
XX
PN MO9928448-A1.
XX
PD 10-JUN-1999.
XX
PF 26-NOV-1998; 98WO-DK00520.
XX
PR 10-JUL-1998; 98DK-0000925.
PR 26-NOV-1997; 97DS-0979673.
PR 30-DEC-1997; 97DK-0001557.
PR 30-JUN-1998; 98DS-0107657.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Lembeck J, Nielsen BR, Nielsen RI;
XX
DR WPI; 1999-404822/34.
XX
DR P-PSDB; AAY23339.
XX
PT New glucoamylase obtained from Talaromyces emersonii
XX
PS Claim 13; Fig 13; 79pp; English.
XX
CC The present sequence represents a glucoamylase gene locus obtained from
CC Talaromyces emersonii. The glucoamylase enzymes have high thermal
CC stability so that a saccharification process may be carried out within
CC a shorter period of time or the process may be carried out using a lower
CC enzyme dosage. The glucoamylase enzymes can be used for saccharifying
CC starch hydrolyzate for converting starch or partially hydrolysed starch
CC into a syrup containing dextrose. They can be used for producing
CC oligosaccharides, specialty syrups, ethanol for fuel, beverages or
CC organic compounds such as citric acid, ascorbic acid, lysine or glutamic
CC acid.
XX
SQ Sequence 2748 BP; 628 A; 815 C; 674 G; 631 T; 0 other;
XX

Alignment Scores:
Pred. No.: 1 32 Length: 2748
Score: 125.50 Matches: 103
Percent Similarity: 31.948 Conservative: 58
Best Local Similarity: 20.448 Mismatches: 182
Query Match: 3.72% Indels: 161
DB: 20 Gaps: 23

US-09-677-653a-50 (1-647) x AAx81820 (1-2748)
QY 40 GlyArgGlnValSerProProAspAsn----- 48
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Db 1370 GGTAGGCAATATGAAATTCCTCCGACAGCGGTGTACTAATTGATTCAGACCTCTGGAA 1429

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Qy 49 -----PheThrAlaAlaGlnAspLeuAlaGlnSerLeuAsp 61
Db 1430 GAAGTAGAAGATCTCTATTCATCCACACCGCGCTGACACACCGCC--CTGGCGAA 1486
Qy 62 AlaAsnThrValThrPheProAlaAsn-----IleSerMetPro 75
Db 1487 GGCAATGCATCGGCAACAAGCGTGAACCAACACGCTCTCAACTGCGCTCTCAGGCCCT 1546
Qy 76 GluPhe-----ArgAsnTrp----- 80
Db 1547 CAGGTCCTCTGTCTCTCGACATCATCTGACCGGATCGTATGTTCTGGCAACTTGGT 1606
Qy 81 AlaLysGlyLysIleAspLeuAspSerIleGlyTrpTyrrPheLysTyrrLeuAsp 100
Db 1607 GGCACGCGGCTGTCCGGCAAGGAGGATTCGATTCTGGAGCATCCACACCTTTGAT 1666
Qy 101 ProAlaGlyAlaThrGlu-----SerAlaArgAlaAlaGlyGlu 113
Db 1667 CCCGCCGAGGCTGTGACACATCGACCTTCAGCCGTGTGCGCCGCTGCGCAAAAT 1726
Qy 114 TyrSerLysIleProAspGlyLeuValLysPheSerValAspAlaGluIleArgGluIle 133
Db 1727 CACAAGGTGTCACCGAC-----TCGTTCCGGAGATATC 1759
Qy 134 TyrAsnGluGluCysProValAlaThrAspValSerValProLeuAspGlyArg----- 151
Db 1760 TATGCGATCACTCAGCATTCGACAGAGGATCTGCCGTGGCAGTC--GGCCGTAACCT 1816
Qy 151 ----- 151
Db 1817 GAGGATGCTTACCAGGCGGGAACCCCTGCTACTGGCCACAGCGGCTCAGAGCAG 1876
Qy 152 -----GlnTrp-----SerLeuSerIlePheSer 159
Db 1877 CTTTACGACGCCATCTACACAGTGAAGAAGATCGGCTCGATATCATCGAGCGTACT 1936
Qy 160 PheProMetPheArgThrAlaTyrrAlaValAlaAsnValGluAsnLysGluMetSer 179
Db 1937 CTGCCATTTTCCAGAAATCTACCTCTGCGCGC--GTGGCACCCTAATCTGTGAC 1993
Qy 180 LeuAspValAlaAsnAspLeuIleGluTrpLeuAsnAsnLeuAlaAspTrp----- 196
Db 1994 TCCACGACTTTCACAGCATCTCTCGGCCGTCACAGCGTATGCTGATGATCTGACT 2053
Qy 197 -----ArgTyrValAlaAspSerGlu-----GlnTrp-IleAsnPheTh 209
Db 2054 ATTGTCGTACGTTTGGCTTAGATCTCAGGTAAAGAAAAAATGAACTAATCTCAGT 2113
Qy 209 AsnAspThrThrTyrrTyrrValArgIleArgValLeuArgProThrTyrrAspValProAs 229
Db 2114 TCTAGAGAAATATCTCTCCCTAGA-----CGGCTCTCTTACCGAACAATTC 2161
Qy 229 PPro-ThrGluGlyLeuValArgThrValSerAspTyrArgLeuThrTyrrLysAla--I 248
Db 2162 CCCGTACAGAGCGACCTCGCTTCTGCTCTGCGCTGACTTGCTGCTGCTCTCTCC 2221
Qy 248 IeThrCysGluAlaAsnMetProThrLeuValAspGlnGlyPheTrpIleGlyGlnT 268
Db 2222 TAACCGCTTGGCCGCGACAGCTCGTCTC----- 2253
Qy 268 TyrAlaLeuThrProThrSerLeuProGlnTyrAspValSerGluAlaTyrrAlaLeuHisT 288
Db 2254 -----CTTGCCTTCTGGGGGCAAGCTCCGCAAGCGCTCCCTGCGCTCTGCT 2302
Qy 288 hrLeuThrPheAlaArgProSerSerAlaAlaLeuAlaPheValTrpAlaGlyLeuP 308
Db 2303 CTGCCACCTTGCACGCGCCCATACAGACGCGTACCAACACGCTGTGGCCAACTCTG 2362
Qy 308 roGlnGly-----GlyThrAlaProAlaGlyLysThrProAlaTrpGluGlnA 323
Db 2363 GCTGTGGAGAGTCAAACACACACCAATAGCGCCCATGACACCATCTCTACCTGTGGCTG 2422
Qy 323 IAserSerGlyLysTyrrLeuThrTrpArgHisAsnGlyThrThrPheProAlaGlySerV 343

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Db 2423 TCACCTTCGACGAATTCGACAGCAGTTTACGGGAGACAAATCTACCGCGGCTCGA 2482
Qy 343 aISerTyrValLeuProGluGlyPheAlaLeuGluArgTyrAspProAsnAspGlySerT 363
Db 2483 TC-----CCCGACTGGGCAACT 2500
Qy 363 rPThrAspPheAlaSerAlaGlyAspThrValThrPheArgGluValAlaValAspGluV 383
Db 2501 GG-----TCCACGGCAGCGGATTCCTCCCTCGGCGC-----GATG 2536
Qy 383 aValValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPheThrValArgValP 403
Db 2537 CTTACACCAACAGCAACCCGCTCTG-----TACGTGACCGTCAATCTGC 2581
Qy 403 rOProSerAsnAlaTyrrThrAsnThrValPheArgAsn-----ThrLeuGlu 419
Db 2582 CCCCTGGCACCAAGCTTCAGTACAAAGTTCTTCAAGAACCAAGACGAGCGGACCATCTGCT 2641
Qy 419 LuThrArgProSerSerArgArgLeuGluLeuProMetProProAlaAspPheGlyGlnT 439
Db 2642 GGGAAAGACGACCGCAACGCGTGTACACGGTC-----CCACGCTACTGTGGGAGA 2692
Qy 439 hrValAla 441
Db 2693 CTACCGCC 2700

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Search completed: February 27, 2003, 05:13:00  
 Job time : 343 secs